

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2005, 09:45:33 ; Search time 2226.25 Seconds
(without alignments)
8496.727 Million cell updates/sec

Title: US-09-996-630A-11_COPY_1_400

Perfect score: 400
Sequence: 1 gctctaaagtgctcaagacc.....ccaaattgatgccaccag 400

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: 1: gb_ba: 2: gb_hgt: 3: gb_in: 4: gb_cm: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_sts: 12: gb_sy: 13: gb_un: 14: gb_vl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	400	100.0	4165	6	AX329586 Sequence
2	398.4	99.6	2193	6	CQ722611 Sequence
3	398.4	99.6	2298	6	AX166529 Sequence
4	398.4	99.6	4772	6	AX642970 Sequence
5	398.4	99.6	4882	9	HUMK1A0
6	398.4	99.6	5519	9	AF226044
7	396.8	99.2	5140	9	BC071567
8	323.8	81.0	4708	10	AF387809
9	322.2	80.5	3004	10	RNSNF1KIN
10	322.2	80.5	3101	10	BC020189
11	275	68.8	248901	2	AC118087
12	212	53.0	143034	9	AC104184
13	212	53.0	106485	2	AC138808
14	208.2	52.0	160170	2	AC143769
15	171.8	43.0	194261	10	AC121264
16	171.8	42.0	206641	10	AC120394
17	168.2	42.0	252055	2	AC106612
18	137.2	34.3	1253	5	BC075868
19	130.8	32.7	2834	5	BC060922

20	107.4	26.9	182002	2	AC142090
21	104.4	26.1	149790	9	AC022106
22	104.4	26.1	157076	9	AC010441
23	104.4	26.1	229053	2	AC010309
24	100.2	25.1	546	9	BC038539
25	80.6	20.1	136547	2	AC134966
26	76.6	19.1	199086	2	CR388073
27	72.6	18.1	2860	6	CQ580679
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29	72.6	18.1	3172	3	AY052073
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34	50	12.5	51	6	CQ001589
35	46.4	11.6	128326	8	AP003756
36	46.4	11.6	157974	8	AP003755
37	43.2	10.8	131711	2	AP003954
38	43.2	10.8	144337	8	AP005320
39	43.2	10.8	152883	8	AP004269
40	43.2	10.8	152883	8	AC084319
41	43	10.5	158574	8	AP003763
42	42	10.5	146458	2	AC134346
43	42	10.5	157009	8	AC137748
44	41.8	10.4	4235	10	BC049083
45	41.8	10.4	104128	10	AL929562

ALIGNMENTS

RESULT 1	AX329586	AX329586	4165 bp	DNA	linear	PAT 09-JAN-2002
LOCUS	AX329586	Sequence 95 from Patent WO0194629.				
DEFINITION	AX329586	AX329586.1 GI:18102564				
ACCESSION	AX329586					
VERSION	AX329586.1	GI:18102564				
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					
REFERENCE						
AUTHORS	Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,					
TITLE	Horrigan, S., Soppet, D.R. and Weaver, Z.					
JOURNAL	Cancer gene determination and therapeutic screening using signature					
FEATURES	gene sets					
source	Patent: WO 0194629-A 95 13-DEC-2001;					
ORIGIN						
Query Match	100.0%; Score 400; DB 6; Length 4165;					
Best local Similarity	100.0%; Pred. No. 2.7e-108;					
Matches	400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 GTCCTAAAGAGTGTAAAGACCTAATTTACACCGAGTCTTACAGAGATCTCCCAAGAGAGGC	60				
DB	1 GTCCTAAAGAGTGTAAAGACCTAATTTACACCGAGTCTTACAGAGATCTCCCAAGAGAGGC	60				
QY	61 TTTCTTTAGAGAGATTGAATATCATCTTGGCTTTCAGAGAGTGGACCTTACACAGTAC	120				
DB	61 TTTCTTTAGAGAGATTGAATATCATCTTGGCTTTCAGAGAGTGGACCTTACACAGTAC	120				
QY	121 AAAGTATACATCTTCCCTGTGTGATACAAAATCTCTCGAAGAGAGACATACATAT	180				
DB	121 AAAGTATACATCTTCCCTGTGTGATACAAAATCTCTCGAAGAGAGACATACATAT	180				
QY	181 CATTCAGCGATGTGCTTGGGACATAGCGATTCAGAGCCATTTAGAACCCCTGGA	240				

Db 181 CATTGACGGCATGTCCTGGGACATAGCGGATCGAGACGATTGTAGAACCCCTGGA 240
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QY 301 AGAAAAGCAAGAGAAAATAACAGACAGATCTGCAAGCCGAGCAATATCAAGGCCCA 360
Db 301 AGAAAAGCAAGAGAAAATAACAGACAGATCTGCAAGCCGAGCAATATCAAGGCCCA 360
QY 361 GTTTAGGCACTCATGGCCAAACCAAAATGATGTAACCCGAG 400
Db 361 GTTTAGGCACTCATGGCCAAACCAAAATGATGTAACCCGAG 400
RESULT 2
CQ722611 2193 bp DNA linear PAT 03-FEB-2004
LOCUS CQ722611 Sequence 8545 from Patent WO02068579.
DEFINITION CQ722611
ACCESSION CQ722611 GI:42283468
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
Venter, C.J., Adams, M.C., Li, P.W., and Myers, E.W.
Kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
Patent: WO 02068579-A 8545 06-SEP-2002;
JOURNAL PE Corporation (NY) (US)
FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 99.8%; Pred. No. 7.9e-108;
Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 609 GTCTAAGAAGTGAAGACCTTAATTAACGGAATGCTACAGAGATCCCAAGAGAGGCG 668
QY 61 TTCTTTAGAAGAGATTGAAAATCATCTTGCTTCAGGAGGTGAGACCCCTTCACAGCTAC 120
Db 669 TTCTTTAGAAGAGATTGAAAATCATCTTGCTTCAGGAGGTGAGACCCCTTCACAGCTAC 728
QY 121 AAAAGTAAACATTCCTCTGTCATACAAAATCTCTCGAAGAGAGACAAACAGCAT 180
Db 729 AAAAGTAAACATTCCTCTGTCATACAAAATCTCTCGAAGAGAGACAAACAGCAT 788
QY 181 CATTGACGGCATGTCCTGGGACATAGCGGATCGAGACGCAATGTAGAACCCCTGGA 240
Db 789 CATTGACGGCATGTCCTGGGACATAGCGGATCGAGACGCAATGTAGAACCCCTGGA 848
QY 241 AACCAACAGGTATTAACCATATTCACGCCACATCTTCCTGCTGGTGAAGAGATCCTGAG 300
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QY 361 GTTTAGGCACTCATGGCCAAACCAAAATGATGTAACCCGAG 400
Db 969 GTTTAGGCACTCATGGCCAAACCAAAATGATGTAACCCGAG 1008

RESULT 3
AX166529 2298 bp DNA linear PAT 22-JUN-2001
LOCUS AX166529 Sequence 20 from Patent WO0138503.
DEFINITION AX166529
ACCESSION AX166529 GI:14546874
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
Plowman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R.,
Plasmgen, P. and Clary, D.S.
Novel human protein kinases and protein kinase-like enzymes
Patent: WO 0138503-A 20 31-MAY-2001;
JOURNAL Sugan, Inc. (US)
FEATURES
source location/Qualifiers
1. 2298
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match 99.6%; Score 398.4; DB 6; Length 2298;
Best Local Similarity 99.8%; Pred. No. 7.9e-108;
Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 61 TTCTTTAGAAGAGATTGAAAATCATCTTGCTTCAGGAGGTGAGACCCCTTCACAGCTAC 120
Db 774 TTCTTTAGAAGAGATTGAAAATCATCTTGCTTCAGGAGGTGAGACCCCTTCACAGCTAC 833
QY 121 AAAAGTAAACATTCCTCTGTCATACAAAATCTCTCGAAGAGAGACAAACAGCAT 180
Db 834 AAAAGTAAACATTCCTCTGTCATACAAAATCTCTCGAAGAGAGACAAACAGCAT 893
QY 181 CATTGACGGCATGTCCTGGGACATAGCGGATCGAGACGCAATGTAGAACCCCTGGA 240
Db 894 CATTGACGGCATGTCCTGGGACATAGCGGATCGAGACGCAATGTAGAACCCCTGGA 953
QY 241 AACCAACAGGTATTAACCATATTCACGCCACATCTTCCTGCTGGTGAAGAGATCCTGAG 300
Db 954 AACCAACAGGTATTAACCATATTCACGCCACATCTTCCTGCTGGTGAAGAGATCCTGAG 1013
QY 301 AGAAAAGCAAGAGAAAATAACAGACAGATCTGCAAGCCGAGCAATATCAAGGCCCA 360
Db 1014 AGAAAAGCAAGAGAAAATAACAGACAGATCTGCAAGCCGAGCAATATCAAGGCCCA 1073
QY 361 GTTTAGGCACTCATGGCCAAACCAAAATGATGTAACCCGAG 400
Db 1074 GTTTAGGCACTCATGGCCAAACCAAAATGATGTAACCCGAG 1113
RESULT 4
AX642970 4772 bp DNA linear PAT 24-FEB-2003
LOCUS AX642970 Sequence 47 from Patent WO01096547.
DEFINITION AX642970
ACCESSION AX642970
VERSION AX642970.1 GI:28550119
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
Yue, H., Lal, P., Bandman, O., Borowsky, M., Au-Young, J., Lu, Y.,
Gandhi, A.R., Tribouley, C.M., Wallis, N., Yao, M.G., Lu, D.A.,
Greenwald, S.R., Ramkumar, J., Griffin, J.A., Kearney, L., Burford, N.,


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RESULT 6
AF226044
LOCUS      AF226044      519 bp      mRNA      linear      PRI 20-JUL-2000
DEFINITION Homo sapiens HSNFRK (HSNFRK) mRNA, complete cds.
ACCESSION  AF226044
VERSION     AF226044.1  GI:9295326
KEYWORDS   FLI CDNA.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 519)
AUTHORS    Li,Y., Wu,T., Xu,S., Ren,S., Chen,Z. and Han,Z.
TITLE      A novel gene expressed in human adrenal gland
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 5519)
AUTHORS    Li,Y., Wu,T., Xu,S., Ren,S., Chen,Z. and Han,Z.
TITLE      Direct Submission
JOURNAL    Submitted (19-JAN-2000) Chinese National Human Genome Center at
Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
Shanghai 201203, P. R. China
LOCATION/Qualifiers
1..5519
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ORIGIN
Query Match      99.6%; Score 398.4; DB 9; Length 5519;
Best Local Similarity 99.8%; Pred. No. 8e-108;
Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GCTTAAAGAGTCTAAAGACCTTAATTACAGGATGCTACAGAGAGATCCCAAGAAAGGC 60
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QY      61  TTCTTAAAGAGATTAAGAAATCATCTTGGCTTCAAGAGATGCGCTTCAACCACTAC 120
DB      1415 TTCTTAAAGAGATTAAGAAATCATCTTGGCTTCAAGAGATGCGCTTCAACCACTAC 1474
QY      121  AAAGTAAACATTCCTCTGTGTGCATACAAAATCTCTCGAAGAGAGACAAACAGCAT 180
DB      1475 AAAGTAAACATTCCTCTGTGTGCATACAAAATCTCTCGAAGAGAGACAAACAGCAT 1534
QY      181  CATTCAGCCGATGCTCTGGGACATAGCGGATCGAGAGCCATTTGTAGAACCTTGG 240
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QY      301  AGAAAAAGCAAGAAAGAAATACAGACCGATCTGCAAGCCCGAGCAATATCAAGGCCCA 360
DB      1655 AGAAAAAGCAAGAAAGAAATACAGACCGATCTGCAAGCCCGAGCAATATCAAGGCCCA 1714
QY      361  GTTTAGGACGATGAGCCCAACCAAAATGATGATCCCGAG 400
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RESULT 7
BC071567
LOCUS      BC071567      5140 bp      mRNA      linear      PRI 25-JUN-2004
DEFINITION Homo sapiens SNF-1 related kinase, mRNA (CDNA clone MGC:87067
ACCESSION  BC071567
VERSION     BC071567.1  GI:47939483
KEYWORDS   MGC.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 5140)
AUTHORS    Strusberg,R.L., Feingold,R.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shennan,C.M., Schuler,G.D.,
Altshul,S.F., Zeeberg,B., Buecaw,K.H., Scheffer,C.F., Bat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carrinci,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.J., Bosak,S.A., McSwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Morley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hilyk,S.W.,
Villalón,D.K., Mizny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahny,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Boutfield,G.G., Blakeley,A.C., Greenwood,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Touchman,J.W., Green,E.D.,
Boutfield,Y.S., Krzywinski,M.I., Skalek,U., Smallus,D.E.,
Scherer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 5140)
Strusberg,R.
Direct Submission
Submitted (01-JUN-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NHI-MGC Project URL: http://mgc.nhi.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shireki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcdexax11.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
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Clome distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILINL at: <http://image.llnl.gov> Series: IRAX Plate: 167 Row: b Column: 13 This clone was selected for full length sequencing because it

FEATURES passed the following selection criteria: matched mRNA gi: 21361642.
Location/Qualifiers

SOURCE

1. .5140

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ORIGIN

Query Match 99.2%; Score 396.8; DB 9; Length 5140;

Best Local Similarity 99.5%; Pred. No. 2.4e-107;

Matches 398; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCCTAAGAGTGTAAAGCTTAATTAACCGGATGCTACAGAGATCCCAAGAGAGGCG 60

DB 958 GTCCTAAGAGTGTAAAGCTTAATTAACCGGATGCTACAGAGATCCCAAGAGAGGCG 1017

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QY 121 AAAGTATTAACATTCCTTGTGTCATCAAAAATCTCTCGAAGAGAGACAACAGCAT 180

DB 1078 AAAGTATTAACATTCCTTGTGTCATCAAAAATCTCTCGAAGAGAGACAACAGCAT 1137

QY 181 CATTCAAGGATGCTGTGGGACATAGCGGATCGAGAGCCCATTTGAAGAGCCCTGGA 240

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QY 301 AGAAAGCAAGAGAAAGAAATATACAGACCATCTTGAAGCCGAGCAATATCAAGGCCCA 360

DB 1258 AGAAAGCAAGAGAAAGAAATATACAGACCATCTTGAAGCCGAGCAATATCAAGGCCCA 1317

QY 361 GTTTAGGAGTCATAGGCCAACCAAAATTGATGATACCCAG 400

DB 1318 GTTTAGGAGTCATAGGCCAACCAAAATTGATGATACCCAG 1357

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QY 1318 GTTTAGGAGTCATAGGCCAACCAAAATTGATGATACCCAG 1357

QY 1318 GTTTAGGAGTCATAGGCCAACCAAAATTGATGATACCCAG 1357

QY 1318 GTTTAGGAGTCATAGGCCAACCAAAATTGATGATACCCAG 1357

QY 1318 GTTTAGGAGTCATAGGCCAACCAAAATTGATGATACCCAG 1357

QY 1318 GTTTAGGAGTCATAGGCCAACCAAAATTGATGATACCCAG 1357

QY 1318 GTTTAGGAGTCATAGGCCAACCAAAATTGATGATACCCAG 1357

QY 1318 GTTTAGGAGTCATAGGCCAACCAAAATTGATGATACCCAG 1357

LOCUS AF387809 4708 bp mRNA linear ROD 13-SEP-2002
DEFINITION Mus musculus strain BALB/c SNF-1 related kinase (Snk) mRNA,
complete cds.

ACCESSION

AF387809

VERSION

AF387809.2

KEYWORDS

SOURCE

ORGANISM

Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

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JOURNAL

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JOURNAL

AF387809 4708 bp mRNA linear ROD 13-SEP-2002
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complete cds.

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VERSION

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KEYWORDS

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DEFINITION Mus musculus strain BALB/c SNF-1 related kinase (Snk) mRNA,
complete cds.

ACCESSION

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VERSION

AF387809.2

KEYWORDS

SOURCE

ORGANISM

Mus musculus

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AUTHORS

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JOURNAL

Db 922 CTCCTCGAAGAGATGAAAGCACACCTTGCTCCAGGAGTGAGACCATCACACGAC 981
QY 121 AAGATTAACATTCCTCCCTTGTGCATACAAAATCTCTGGAGAGAGACAAACAGCAT 180
Db 982 CAAATTAACATTCCTCCCTTGTGCATACAAAATCTCTGGAGAGAGACAAACAGCAT 1041
QY 181 CATTACGCCATGCTGCTGGAGACATAGCGGATTCAGACGCGCATTTGTAAGACCTTGA 240
Db 1042 CATTACGCCATGCTGCTGGAGACATAGCGGATTCAGACGCGCATTTGTAAGACCTTGA 1101
QY 241 AACCAACAGGTATACCATATACACGCCACATCTCTGCTGCTGAAAGATCTTGA 300
Db 1102 AACCAACAGGTATACCATATACACGCCACATCTCTGCTGCTGAAAGATCTTGA 1161
QY 301 AGAAAAGCAGAGAGAAATACAGACCGATTCGAGCGCCGAGCAATATCAAGGCCA 360
Db 1162 AGAAAAGCAGAGAGAAATACAGACCGATTCGAGCGCCGAGCAATATCAAGGCCA 1221
QY 361 GTTTAGCAGTCATGCGCAACCAAAATTGATGTACCCA 399
Db 1222 GTTTAGCAGTCATGCGCAACCAAAATTGATGTACCCA 1260

RESULT 9
RNSNF1KIN 3004 bp mRNA 1linear ROD 29-FEB-1996
LOCUS R.norvegicus mRNA for SNF1-related kinase.
DEFINITION X89383
VERSION X89383.1 GI:1213223
KEYWORDS SNF1-related kinase; snrk gene.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1
REFERENCE
AUTHORS Becker, W., Heukelbach, J., Kentrup, H. and Joost, H.G.
TITLE Molecular cloning and characterization of a novel mammalian protein kinase harboring a homology domain that defines a subfamily of serine/threonine kinases
JOURNAL Eur. J. Biochem. 235 (3), 736-743 (1996)
MEDLINE 96184553
PUBMED 8654423
REFERENCE 2 (bases 1 to 3004)
AUTHORS Heukelbach, J.
TITLE Direct Submission
JOURNAL Submitted (03-JUL-1995) J. Heukelbach, Institut fuer Pharmakologie und Toxik., der RWTH Aachen, Wendlingweg 2, D-52057 Aachen, FRG
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FSNKPQPKRLTTSVCSGLAYSAPEILLGDEYDAPADIVSLGIVLIMLVCGQPPQEA

ORIGIN
Query Match 80.5%; Score 322.2; DB 10; Length 3004;
Best Local Similarity 88.0%; Pred. No. 4,8e-85;
Matches 351, Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 1 GTCTAAAGAGTGTAAAGACCTTAATTACACGATGCTACAGAGATGCCAAGAAAGGC 60
Db 863 GTCTCAGGGGTACAGGACCTCATCACGAGTGTGACAGAGAGACCCAAAAGGAGAC 922
QY 61 TCTTTAGAGAGATTGAAATCATCCTTGCTGACAGGAGTGAACCTTCAACAGCTAC 120
Db 923 CTCCTCGAAGAGATTGAAAGCACCTTGTGCTCAAGAGAGTGAACCTTCAACAGCCAC 982
QY 121 AAGATTAACATTCCTCCCTTGTGCATACAAAATCTCTGGAAGAGACAGACAGCAT 180
Db 983 CAAATTAACATTCCTCCCTTGTGCATACAAAATCTCTGGAAGAGAGACAGATAGCAT 1042
QY 181 CATTACGCCATGCTGCTGGAGACATAGCGGATTCAGACGCGCATTTGTAAGACCTTGA 240
Db 1042 CATTACGCCATGCTGCTGGAGACATAGCGGATTCAGACGCGCATTTGTAAGACCTTGA 1102
QY 241 AACCAACAGGTATACCATATACACGCCACATCTCTGCTGCTGAAAGATCTTGA 300
Db 1103 AACCAACAGGTATACCATATACACGCCACATCTCTGCTGCTGAAAGATCTTGA 1162
QY 301 AGAAAAGCAGAGAGAAATACAGACCGATTCGAGCGCCGAGCAATATCAAGGCCA 360
Db 1163 AGAAAAGCAGAGAGAAATACAGACCGATTCGAGCGCCGAGCAATATCAAGGCCA 1222
QY 361 GTTTAGCAGTCATGCGCAACCAAAATTGATGTACCCA 399
Db 1223 GTTTAGCAGTCATGCGCAACCAAAATTGATGTACCCA 1261

RESULT 10
BC020189 3101 bp mRNA 1linear ROD 29-JUN-2004
LOCUS Mus musculus SNF related kinase, mRNA (cDNA clone MGC:28970
DEFINITION IMAGE:4482701), complete cds.
ACCESSION BC020189
VERSION BC020189.1 GI:18043575
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3101)
REFERENCE
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, K.H., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheffer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Datchenko, L., Matusins, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uedl, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abrahamson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Vahney, U., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
JOURNAL
TITLE
JOURNAL

REMARK
COMMENT

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2 (bases 1 to 3101)
Strusberg, R.
Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgapb-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (ILNL)
BC Cancer Agency, Vancouver, BC, Canada
Info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Motin, Taka Olson, Diana Palmquist, Anca Petrescu, Anna Lissa Prabh, Parvaneh Saeedi, Jr Santos, Angelique Schnerch, Ursula Skalska, Duane Smilun, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAX Plate: 38 Row: b Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19526941.
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/clone="MGC:28970 IMAGE:4482701"
/tissue_type="mammary tumor. Metallochionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy."
/clone_id="NCI CGAP_Mam1"
/lab_host="DH10B"
/note="vector: pCMV-SPORT6"
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FSNKFQGGKLTSGSLAYAPBILIGDEYDPAVDIMGLVILFWLVCQPPQPA
NDSTLTMDKCTVPRVSAGCRDLITMLQDPKRRASLEIESHPMLQCTDPS
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RIIREKQKEIQTSAESPNIKAQFQSQWPKTDVQDLDDLTATPLSHATVQSA
RAGNDVNLGHSKGLCDPAKDELPELAGPALSTVPASMKPKAGKCLFVDEDE
EEDBKPVLSITQVLRKPSVTNRLSRKSAFLVNOIFEEGSGDEPMDENLPK
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RDSSEGRPSGEGCGSKPSGGGCVKASBEGCTGGCGSGGCTPSTGASRRC

ORIGIN

Query Match 80.5%; Score 322.2; DB 10; Length 3101;
Best Local Similarity 88.0%; Pred. No. 4,8e-85;
Matches 351; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

AGDSSSPSPASAA PRGAELVQSLVSLGSGQHLGKATLLDPOKALFSSVQOE
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PASCCHVT"

QY 1 GCTTAAAGAGTGTAAAGACCTTAATTAACGAGATGCTACAGAGAGATCCCAAGAGAGG 60
DB 904 GTCTGACGGGTGACGAGGACCTGATACAGAAATGCTACAGAGAGAGAGAGAGG 963
QY 61 TTCTTTGAAGAGATTGAATATCATCTTGGCTTACAGAGAGTGAACCTTACCAGTAC 120
DB 964 CTCTCTGGAAGAATGTAAGACCCCTTGGCTTACAGAGAGTGAACCCATCACAGCAC 1023
QY 121 AAGATATACATTCCTTGTCTATACAAATCTCTGGAAGAGAGAGAGAGAGAGAT 180
DB 1024 CAGGTATACATTCCTTGTCTATACAAATCTCTGGAAGAGAGAGAGAGAGAGAT 1083
QY 181 CATTACGCGATGCTGCTTGGGAGACATACGAGATGAGAGAGAGAGAGAGAGAT 240
DB 1084 CATTACGCGATGCTGCTGCGGAGACATACGAGAGAGAGAGAGAGAGAGAT 1143
QY 241 AACCAAGGTATACATTCATACAGAGAGATCTTCTGCTGGAAGAGAGATCTGAG 300
DB 1144 AACCAAGGTATACATTCATACAGAGAGATCTTCTGCTGGAAGAGAGATCTGAG 1203
QY 301 AGAAAGCAAGAGAAAGAAATACAGACAGATCTGCAAGCGGCAATATCAAGGCCA 360
DB 1204 AGAAAGCAAGAGAAAGAAATACAGACAGATCTGCTGAGCCCAAGCAATCAAGGCCA 1263
QY 361 GTTTAGGCACTGATGGCCAAACAAATGATGATGCCCA 399
DB 1264 GTTTAGGCACTGATGGCCAAACAAATGATGATGCCCA 1302

FEATURES
SOURCE

RESULT 11
AC118087/c
LOCUS
DEFINITION
Rattus norvegicus clone CH230-38M5, *** SEQUENCING IN PROGRESS ***
3 unordered pieces.
AC118087
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 248901)
Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Albrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Ayagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A.,
Chacho, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Gree, A., D'Souza, L.,
Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Bayes, K.,
Egan, A., Escoto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
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Frazer, C.M., Gabi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebreyes, E., Geer, K., Gili, R., Grady, M., Guerra, M., Guevara, W.,
Gunnarste, P., Heald, W., Hamill, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlik, P., Hawes, A., Henderson, N., Hernandez, J.,
Henderson, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M.,
Hollins, B., Howells, S., Huylk, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,

REFERENCE
AUTHORS

1 (bases 1 to 248901)
Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Albrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Ayagi, A., Ayodeji, M., Baca, E., Baden, H.,
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Gunnarste, P., Heald, W., Hamill, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlik, P., Hawes, A., Henderson, N., Hernandez, J.,
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Hollins, B., Howells, S., Huylk, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,

Karpthy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowals, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensen, L., Louie, H., Lozano, R. J., Lu, X., Ma, J., Maheshwari, M., Mahdian, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaelelem, O., Okunolu, G., Olarunmugbon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Pu, M., Pu, M., Quirio, J., Rachlin, E., Reeves, K., Regier, M. A., Reid, R., Reilly, B., Reilly, M., Ren, Y., Reuter, R., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, M., Saverly, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C. D., Smajic, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soes, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabori, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villanar, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wood, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstein, G., and Gibbs, R. A.

Direct Submission
Unpublished
2 (bases 1 to 248901)
Worley, K. C.

Direct Submission
Submitted (13-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 248901)

Rat Genome Sequencing Consortium.
Direct Submission
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23194785. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rac/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Project name: GUPK
Center project name: CH230-38MS
Center clone name: CH230-38MS

----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 230944 bases at least Q40
Consensus quality: 233870 bases at least Q30
Consensus quality: 23397 bases at least Q20
Estimated insert size: 239916, sum-of-contigs estimation
Quality coverage: 5x in Q20 bases, sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 74533: contig of 74533 bp in length
74534 74633: gap of unknown length
74634 234493: contig of 159860 bp in length
234494 234593: gap of unknown length
234594 248901: contig of 14308 bp in length.

Location/Qualifiers
1.248901
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-38MS"
157891..158713
/note="clone boundary
clone_end:17
site:
end_sequence:BH281110"

ORIGIN

Query Match 68.8%; Score 275; DB 2; Length 248901;
Best Local Similarity 85.2%; Pred. No. 6.9e-71;
Matches 323; Conservative 0; Mismatches 45; Indels 11; Gaps 1;

QY 21 TATTACACGAGTCTACAGAGATCCCAAGAGAGGCTCTTAGAGAGATTGANA 80
|||
DB 60350 TATTACACGAGTCTGCGAGAGAGACCCCAAGAGAGGCTCTGTAAGAGATTGANA 60291

QY 81 ATCATCTCTGCTTCAAGAGAGTGAACCTTCAACAGCTACAAAGTATACATTCCTG 140
60290 GCCACCTTGGCTCCAGAGAGTGAACCTTCAACAGCTACAAAGTATACATTCCTG 60231

QY 141 TGTCTATCAAAAATCTCTCGAAGAGAGACACACATCATTCAGCGCATGCTG 200
60230 TGTCTATCAAAAATCTCTCGAAGAGAGACACACATCATTCAGCGCATGCTG 60182

QY 201 GGGACATAGCGATGGAAGAGCGCATTTGAGAGCCCTGGAACCAACAGATTAACCA 260
60181 GGGACATAGCGATGGAAGAGCGCATTTGAGAGCCCTGGAACCAACAGATTAACCA 60122

QY 261 TCACAGCCACATCTCTGCTGCTGCTGAAGGATCCTGAGAGAAAAGCAAGAAA 320
60121 TCACAGCCACATCTCTGCTGCTGCTGAAGGATCCTGAGAGAAAAGCAAGAAA 60062

QY 321 TCACAGCCACATCTGCAAGCCGAGCATATCAAGCCCAAGTTAGGCGATGATGCC 380
60061 TCACAGCCACATCTGCAAGCCGAGCATATCAAGCCCAAGTTAGGCGATGATGCC 60002

QY 381 CCAAAATGATGATACCCCA 399
DB 60001 CTAATAATGATGATACCCCA 59983

RESULT 12
AC104184
LOCUS AC104184 143034 bp DNA linear PRI 23-MAR-2002
DEFINITION Homo sapiens chromosome 3 clone RP11-188P20, complete sequence.
AC104184 AC027581
AC104184.2 GI:19697457
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 143034)
Kaul, R. K., Olson, M. V., Zhou, Y., James, R. A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K. A., Raymond, C. and Haugen, E. D.

TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 143034)
 AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
 TITLE Direct Submission
 JOURNAL Submitted (06-DEC-2001) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA
 REFERENCE 3 (bases 1 to 143034)
 AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
 Saenphitumachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
 TITLE Direct Submission
 JOURNAL Submitted (23-MAR-2002) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA
 COMMENT On Mar 23, 2002 this sequence version replaced gi:11786316.

----- Genome Center
 Center: University of Washington Genome Center
 Center Code: UWGC
 Web site: <http://www.genome.washington.edu>
 Contact: uwgchgs@u.washington.edu
 Drafting Center: BCM

----- Project Information
 Center project name: chr-3
 Center clone name: Rp11-188P20 (bc0291)

----- Summary Statistics

Sequencing vector: plasmid; 108752; 42% of reads
 Chemistry: Dye-terminator ET; 67% of reads
 Chemistry: Dye-terminator Big Dye; 33% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 142918 bases at least Q40
 Consensus quality: 143028 bases at least Q30
 Consensus quality: 143034 bases at least Q20
 Insert size: 142838; sum-of-contigs
 Quality coverage: 8.0x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5': Mapping in progress
 3': Rp11-258N2 (UWGC:bc0637) AC024378

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

ECORI

HindIII

BglII

SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
-----	-----	-----	-----	-----	-----
-----	-----	-----	-----	-----	-----

8696	8704	1129	1114	10270	10243
6	<800	6382	6515	2067	2063
2882	2945	512	<800	5480	5668
2540	2530	449	<800	3606	3574
3643	3781	2552	2517	928	930
1514	1486	3416	3369	365	<800
631	<800	7168	7307	7579	7709
865	847	1854	1889	782	<800
2055	2049	1696	1655	4596	4559
909	897	397	<800	2776	2784
3796	3781	2926	2977	184	<800
5481	5462	4712	4619	2132	2156
1935	1951	45	<800	856	867
507	<800	825	895	659	<800
120	<800	5281	5260	1899	1874
1153	1139	4614	4619	1261	1259
2641	2663	2273	2249	2817	2784
2145	2184	2075	2065	6712	6648
1526	1486	14383	14415	128	<800
1000	997	10039	9940	4209	4192
1126	1139	8620	8673	46	<800
1649	1651	501	<800	2157	2156
637	<800	11469	11355	6593	6648
788	<800	1883	1889	6080	6248
18870	19027	4982	4848	3363	3421
1312	1314	1943	1889	5134	5104
172	<800	886	895	5754	5668
3298	3303	881	895	4281	4192
1332	1314	85	<800	4197	4192
5959	5917	4281	4178	3177	3210
10560	10431	593	<800	9088	9070
7179	7208	66	<800	150	<800
3985	4046	3551	3581	2704	2784
9799	9561	488	<800	3282	3210
4653	4680	5651	5589	708	<800
1150	1139	2443	2517	8040	8083

```
-----
764      7701      1249      1229      3827      3766
-----
5866      5917      4839      4848      228      <800
-----
1182      1139      1244      1229      662      <800
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1154      1139      185      <800      4221      4192
-----
973      997      1386      1353      9761      9678
-----
2345      2368      2602      2517      1167      1161
-----
225      <800      1492      1453      7807      7709
-----
326      <800      2460      2517
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2508      2530      72      <800
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6154      6119      7817      7816
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567      <800      4142      4178
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1085      1139      345      <800
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2044      2049      2849      2895
-----
473      <800
-----
2553      2530
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source
1. .143034
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/clone="RP11-188P20"
/clone_lib="RP11 human BAC library 11"
ORIGIN
Query Match      53.0%; Score 212; DB 9; Length 143034;
Best Local Similarity 93.6%; Pred. No. 4.7e-52;
Matches 221; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY      19      CCTAATTACACGGATGCTACAGAGATCCCAAGAGAGGGCTTTTGAAGAGATTGA 78
DB      63915  CCTAATCACACGGATGCTACAGAGATCCCAAGAGAGGGCTTTTGAAGAGATTGA 63974
QY      79      AATATCATCTTGCGCTTCAGGAGTGAACCTTCACAGCTACAAAGTATTAATCCCT 138
DB      63975  AATATCATCTTGCGCTTCAGGAGTGAACCTTCACAGCTACAAAGTATTAATCCCT 64034
QY      139  TGTGTATACAAAATCTCTCGAAGAGAGACAAACAGCATATTCAAGCGATGGTCT 198
DB      64035  TGTGTATACAAAATCTCTCGAAGAGAGACAAACAGCATATTCAAGCGATGGTCT 64094
QY      199  TGGGACATATAGCGGATCGAGACGCCATTGTAGAAGCCCTGGAAACCAACAGGTATA 254
DB      64095  TGGGACATATAGCGGATCGAGACGCCATTGTAGAAGTACGTCAATGCCGTCAGTACA 64150

RESULT 13
AC138808/c      186485 bp      DNA      linear      HTG 21-JAN-2003
DEFINITION      Homo sapiens chromosome 5 clone RP11-1026L22, WORKING DRAFT
SEQUENCE, 5 unordered pieces.
AC138808
AC138808.1      GI:27805220
VERSION      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
```

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REFERENCE      1 (bases 1 to 186485)
AUTHORS      DOE Joint Genome Institute.
TITLE      Sequencing of Human Chromosome 5
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 186485)
AUTHORS      DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL      Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1688774
Center Clone name: RP11-11_1026L22
-----
Summary Statistics
Consensus quality: 182487 bases at least Q40
Consensus quality: 183346 bases at least Q30
Consensus quality: 183866 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 186085; sum-of-contigs estimation
Quality coverage: 9.4 in Q20 bases; agarose-fp estimation
Quality coverage: 8.84 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1      1126: contig of 1126 bp in length
*      1127      1226: gap of unknown length
*      1227      2350: contig of 1124 bp in length
*      2351      2450: gap of unknown length
*      2451      3522: contig of 1072 bp in length
*      3523      3622: gap of unknown length
*      3623      11173: contig of 7551 bp in length
*      11174      11273: gap of unknown length
*      11274      186485: contig of 175212 bp in length.
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-1026L22"
/clone_lib="RP11 human BAC library 11"
ORIGIN
Query Match      53.0%; Score 212; DB 2; Length 186485;
Best Local Similarity 93.6%; Pred. No. 4.7e-52;
Matches 221; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY      19      CCTAATTACACGGATGCTACAGAGATCCCAAGAGAGGGCTTTTGAAGAGATTGA 78
DB      132476  CCTAATCACACGGATGCTACAGAGATCCCAAGAGAGGGCTTTTGAAGAGATTGA 132417
QY      79      AATATCATCTTGCGCTTCAGGAGTGAACCTTCACAGCTACAAAGTATTAATCCCT 138
DB      132416  AATATCATCTTGCGCTTCAGGAGTGAACCTTCACAGCTACAAAGTATTAATCCCT 132357
QY      139  TGTGTATACAAAATCTCTCGAAGAGAGACAAACAGCATATTCAAGCGATGGTCT 198
DB      132356  TGTGTATACAAAATCTCTCGAAGAGAGACAAACAGCATATTCAAGCGATGGTCT 132297
QY      199  TGGGACATATAGCGGATCGAGACGCCATTGTAGAAGCCCTGGAAACCAACAGGTATA 254
DB      132296  TGGGACATATAGCGGATCGAGACGCCATTGTAGAAGTACGTCAATGCCGTCAGTACA 132241
```

RESULT 14
LOCUS AC143769 160170 bp DNA linear HTG 09-APR-2003
DEFINITION Macaca mulatta clone CH250-270D6, *** SEQUENCING IN PROGRESS ***.
AC143769
AC143769.1 GI:29649247
VERSION HTG: HTGS PHASE2; HTGS_PGI.
KEYWORDS Macaca mulatta (rhinus monkey)
SOURCE Macaca mulatta
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.
1 (bases 1 to 160170)
Poulos, M. and Milosavljevic, A.
Pooled genomic indexing (PGI): mathematical analysis and experiment design
(in) Gulgo, R. and Gusfield, D. (Eds.);
ALGORITHMS IN BIOINFORMATICS, SECOND INTERNATIONAL WORKSHOP, WABI 2002, ROME, ITALY, SEPTEMBER 17-21, 2002, PROCEEDINGS: 10-26; Springer (2002)
2 (bases 1 to 160170)
Milosavljevic, A., Sodergren, E., Casuso, M., Li, B., Jackson, A.R., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaralunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbarta, J., Benton, V., Bimaga, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Briveva, M., Brown, E., Brown, M., Bryant, N.P., Buha, C., Burck, P., Burrell, C., Burrell, K.L., Byrd, N.C., Caron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavous, C., Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Dem, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Egan, A., Barnhart, C., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, J., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guera, W., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogue, M., Holloway, C., Hollins, B., Homel, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W., Louiege, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapa, P., Marondel, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Metzger, M., Miller, A., Miner, G., Miner, Z., Mitchell, T., Monabadi, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokkwo, S., Oguh, M., Okunolu, G., Otagunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Pirmas, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Saverly, G., Scherer, S., Scott, G., Shen, H., Shim, C., Sinoigntari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, K., Stone, H., Sutton, A., Svatek, A., Taber, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Teliro, B., Thomas, N., Thomas, S., Usmani, K., Vaequez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wlezyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorilla, S., Zuberlapati, R., Weinstein, G. and Gibbs, R.
Unpublished
Direct Submission
3 (bases 1 to 160170)
Worley, K.C.
Submitted (09-APR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
----- Genome Center

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: LA50
Center clone name: CH250-270D6
----- Summary Statistics
Chemistry: Dye-primer Bodipy: inf of reads
Chemistry: Dye-terminator Big Dye: inf of reads
Consensus quality: 9954 bases at least Q40
Consensus quality: 11529 bases at least Q30
Consensus quality: 13142 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
* NOTE: The contigs are based on the application
* of the PGI method using the Human genome (NCBI build 31)
* as the comparative genome.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 160170: contig of 160170 bp in length.
Location/Qualifiers
1. 160170
/organism="Macaca mulatta"
/mol_type="genomic DNA"
/db_xref="taxon:9544"
/clone="CH250-270D6"
1. 160170
/note="assembly name: CH250-270D6.1B"
CONFIDENCE: 0.83"

ORIGIN
Query Match 52.0%; Score 208.2; DB 2; Length 160170;
Best Local Similarity 98.6%; Pred. No. 6.5e-51;
Matches 210; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 19 CTTAATTCACGCGATCTCAAGAGATCCCAAGAGAGGCTCTTTAGAGAGATTGA 78
112823 CTTGATACACGCGATCTCAAGAGATCCCAAGAGAGGCTCTTTAGAGAGATTGA 112882
QY 79 AATTCATCTTGGCTTCAGGAGATGACCTTACGAGTACAAAGTATACATTCCTCC 138
112883 AATTCATCTTGGCTTCAGGAGATGACCTTACGAGTACAAAGTATACATTCCTCC 112942
QY 139 TGTGTCAACAATAATCTCTCGAAGAGAGCAACAAGCATTCAGCGCATGTGCT 198
112943 TGTGTCAACAATAATCTCTCGAAGAGAGCAACAAGCATTCAGCGCATGTGCT 113002
DB 199 TGGGACATATGCGGATCGAGACCCCATTTGTA 221
113003 TGGGACATATGCGGATCGAGACCCCATTTGTA 113035

RESULT 15
LOCUS AC121264 194261 bp DNA linear ROD 13-APR-2004
DEFINITION Mus musculus chromosome 9, clone RP24-23JF22, complete sequence.
AC121264
AC121264.8 GI:46360003
VERSION HTG.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 194261)

AUTHORS Birren, B., Nusbaum, C. and Lander, E.
 TITLE Mus musculus chromosome 9, clone RP24-233P22
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 194261)
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barna, N., Baetien, V., Bloom, T., Boguslavsky, L., Boukigalter, B., Brown, A., Camarata, J., Campoliano, A., Chang, J., Chazaro, R., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dekrellano, K., Dewar, K., Diaz, J., Dodge, S., Fero, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hages, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R., Landers, T., Lehoczeky, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Margus, N., Matthews, L., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Menues, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Roselli, M., Roy, A., Santos, R., Schauer, S., Schnupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Sudramanian, A., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE Direct Submission
 JOURNAL Submitted (16-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 REFERENCE 3 (bases 1 to 194261)
 AUTHORS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Baetien, V., Bloom, T., Boguslavsky, L., Boukigalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dekrellano, K., Diaz, J., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hages, N., Hagopian, D., Hages, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Menues, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schnupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE Direct Submission
 JOURNAL Submitted (11-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 REFERENCE 4 (bases 1 to 194261)
 AUTHORS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Baetien, V., Bloom, T., Boguslavsky, L., Boukigalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dekrellano, K., Diaz, J., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hages, N., Hagopian, D., Hages, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, R., McCarty, M., Meldrim, J., Menues, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schnupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 JOURNAL Direct Submission
 COMMENT Submitted (13-APR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence.submissions@road.mit.edu
 Project information
 Center project name: L21224
 Center clone name: 233_F_22

Some of the sequence contained within base pairs 175167 to the end of the clone was stolen from accession AC108846 [WICGR Project L21006].

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DB 33270 AAGCCACCTTGCTGAGGAGTGACCTTCACGCTACAAAGTATTAATCCCT 33329
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QY 199 TGGGACATAGCGGATGAGACCGCATTTGAAAGCCCTGAAACCAACAGATTAAACA 258
DB 33390 CGGGACATAGCGGATGAGACCGCATTTGAAAGCCCTGAAACCAACAGATTAAACA 33449
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Job time : 2231.25 sec

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2005, 09:45:33 ; Search time 2037.02 Seconds
(without alignments)
8496.727 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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1: gb_ba:*
2: gb_hng:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	366	100.0	1641	AK026013	AK026013 Homo sapi
2	366	100.0	3361	AK025449	AK025449 Homo sapi
3	366	100.0	4165	AX329586	AX329586 Sequence
4	366	100.0	4882	HUMK1AAQ	D43636 Human mRNA
5	366	100.0	5140	BC071567	BC071567 Homo sapi
6	366	100.0	5519	AF226044	AF226044 Homo sapi
7	366	100.0	143034	AC104184	AC104184 Homo sapi
8	366	100.0	186485	AC138808	AC138808 Homo sapi
9	358	97.8	2580	G07259	G07259 human STS
10	300	82.0	396	AX337742	AX337742 Sequence
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12	149.6	40.9	253055	AC106612	AC106612 Rattus no
13	132.2	36.1	4708	AF387809	AF387809 Mus muscu
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15	132.2	36.1	194261	AC121264	AC121264 Mus muscu
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21	86.6	23.7	232882	2	AC128448	AC128448 Rattus no
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25	71.4	19.5	248901	2	AC118087	AC118087 Rattus no
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27	54	14.8	250743	3	AE014836	AE014836 Plasmodu
28	53.8	14.7	159109	2	CR376766	CR376766 Danto rer
29	53.8	14.7	179354	2	CR354588	CR354588 Danto rer
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42	51	13.9	125674	2	AP002018	AP002018 Homo sapi
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ALIGNMENTS

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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AK026013.1 GI:10438715
AK026013 Homo sapiens (human)
Oligo capping, fis (full insert sequence).
Homo sapiens (human)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1
Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Ohashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1641)
Sugano, S., Suzuki, Y., Ota, T., Ohashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.
Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: f1cdna@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286, Fax: 81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing. Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing; Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by science and Technology Agency).

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TITLE
JOURNAL
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REFERENCE
AUTHORS
JOURNAL
TITLE

Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKenney, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Mortley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huliyil, S.W.,
Vallalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Raney, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfield, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 5140)
Strausberg, R.
Direct Submission
Submitted (01-JUN-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT
Contact: MGC help desk
Email: cgaaps-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shitaki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www.sngc.stanford.edu>
Contact: (Dickson, Mark) mcdpaxil@stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

FEATURES
source
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAX Plate: 167 Row: b Column: 13
This clone was selected for full length sequencing because it
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DB 4939 ACCGAATTAAGATTAATCCCTACCAAGTGAATTAATGATGTGTGAAGGGGTACAGAT 4998
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DB 5119 AGCAAT 5124

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VERSION AF226044.1 GI:9295326
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 5519)
AUTHORS Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.
TITLE A novel gene expressed in human adrenal gland
JOURNAL Unpublished
2 (bases 1 to 5519)
REFERENCE 2 (bases 1 to 5519)
AUTHORS Li, Y., Wu, T., Xu, S., Ren, S., Chen, Z. and Han, Z.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-2000) Chinese National Human Genome Center at
Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
Shanghai 201203, P. R. China
Location/Qualifiers

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507	<800	825	895	659	<800
120	<800	5281	5260	1899	1874
1153	1139	4614	4619	1261	1259
2661	2663	2273	2249	2817	2784
2145	2184	2075	2065	6712	6648
1526	1486	14383	14415	128	<800
1000	997	10039	9940	4209	4192
1126	1139	8620	8673	46	<800
1649	1651	501	<800	2157	2156
637	<800	11469	11355	6593	6648
788	<800	1883	1889	6080	6248
18870	19027	4982	4848	3363	3421
1312	1314	1943	1889	5134	5104
172	<800	886	895	5754	5668
3298	3303	881	895	4281	4192
1332	1314	85	<800	4197	4192
5959	5917	4281	4178	3177	3210
10560	10431	593	<800	9088	9070
7179	7208	66	<800	150	<800
3955	4046	3551	3581	2704	2784
9799	9561	488	<800	3282	3210
4653	4680	5651	5589	708	<800
1150	1139	2443	2517	8040	8083
7764	7701	1249	1229	3827	3766
5866	5917	4839	4848	228	<800
1182	1139	1244	1229	662	<800
1154	1139	185	<800	4221	4192
973	997	1386	1353	9761	9678
2345	2368	2602	2517	1167	1161

-----	-----	-----	-----	-----	-----
225	<800	1492	1453	7807	7709
326	<800	2460	2517	-----	-----
2508	2530	72	<800	-----	-----
6154	6119	7817	7816	-----	-----
567	<800	4142	4178	-----	-----
1085	1139	345	<800	-----	-----
2044	2049	2849	2895	-----	-----
473	<800	-----	-----	-----	-----
2553	2530	-----	-----	-----	-----
-----	-----	-----	-----	-----	-----
FEATURES	Location/Qualifiers	-----	-----	-----	-----
source	1. 143034	-----	-----	-----	-----
	/organism="Homo sapiens"	-----	-----	-----	-----
	/mol_type="genomic DNA"	-----	-----	-----	-----
	/db_xref="taxon:9606"	-----	-----	-----	-----
	/chromosome="3"	-----	-----	-----	-----
	/clone="RP11-188P20"	-----	-----	-----	-----
	/clone_11b="RP11 human BAC library 11"	-----	-----	-----	-----
ORIGIN	-----	-----	-----	-----	-----
Query Match	100.0%; Score 366; DB 9; Length 143034;	-----	-----	-----	-----
Best Local Similarity	100.0%; Pred. No. 7e-65;	-----	-----	-----	-----
Matches 366; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	-----	-----	-----	-----
QY	1 CCCTTAACCTGCTCTCAAAAGTTCATATAGTACAGTAGTGTATTAATAATATGTCG 60	-----	-----	-----	-----
DB	74401 CCCTTAACCTGCTCTCAAAAGTTCATATAGTACAGTAGTGTATTAATAATATGTCG 74460	-----	-----	-----	-----
QY	61 GAAAAACAGCTCTGATATTTTCTGATGCTGTATATATATTAATATGTAAGTCTGAC 120	-----	-----	-----	-----
DB	74461 GAAAAACAGCTCTGATATTTTCTGATGCTGTATATATATTAATATGTAAGTCTGAC 74520	-----	-----	-----	-----
QY	121 AATTCATCTGTATTTAAAGATGTGACATCTTGACACCAATTTTAAGATAGCTGTGAG 180	-----	-----	-----	-----
DB	74521 AATTCATCTGTATTTAAAGATGTGACATCTTGACACCAATTTTAAGATAGCTGTGAG 74580	-----	-----	-----	-----
QY	181 ACCGAATTAAATATATCCCTACCAAGTGAATAATGATGTGTAAAGGGGTACAGAT 240	-----	-----	-----	-----
DB	74581 ACCGAATTAAATATATCCCTACCAAGTGAATAATGATGTGTAAAGGGGTACAGAT 74640	-----	-----	-----	-----
QY	241 TATCACTGATTTGGTCAGTCTCTCAATGCTGGTGTATTTCCCTCATTTGTGTAACAT 300	-----	-----	-----	-----
DB	74641 TATCACTGATTTGGTCAGTCTCTCAATGCTGGTGTATTTCCCTCATTTGTGTAACAT 74700	-----	-----	-----	-----
QY	301 TGACAGTATGTGACAAATGGGAAAAAATCCAAATATTAAGTACATATTTGTTGTTTC 360	-----	-----	-----	-----
DB	74701 TGACAGTATGTGACAAATGGGAAAAAATCCAAATATTAAGTACATATTTGTTGTTTC 74760	-----	-----	-----	-----
QY	361 AGCAAT 366	-----	-----	-----	-----
DB	74761 AGCAAT 74766	-----	-----	-----	-----
RESULT 8	-----	-----	-----	-----	-----
AC138808/c	AC138808 186485 bp DNA linear HTG 21-JAN-2003	-----	-----	-----	-----
LOCUS	Homo sapiens chromosome 5 clone RP11-1026L22, WORKING DRAFT	-----	-----	-----	-----
DEFINITION	SEQUENCE, 5 unordered pieces.	-----	-----	-----	-----
ACCESSION	AC138808	-----	-----	-----	-----
VERSION	AC138808.1 GI:27805220	-----	-----	-----	-----
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.	-----	-----	-----	-----
SOURCE	Homo sapiens (human)	-----	-----	-----	-----
ORGANISM	Homo sapiens	-----	-----	-----	-----
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	-----	-----	-----	-----

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 186485)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
2 (bases 1 to 186485)
DOE Joint Genome Institute.
Direct Submission
Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1688774
Center clone name: RPCT-11_1026L22

Summary Statistics
Consensus quality: 182487 bases at least Q40
Consensus quality: 183346 bases at least Q30
Consensus quality: 183866 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 166085; sum-of-contigs estimation
Quality coverage: 9.4 in Q20 bases; agarose-fp estimation
Quality coverage: 8.94 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1126: contig of 1126 bp in length
* 1127 1226: gap of unknown length
* 1237 2350: contig of 1124 bp in length
* 2351 2450: gap of unknown length
* 2451 3522: contig of 1072 bp in length
* 3523 3623: gap of unknown length
* 3623 11173: contig of 7551 bp in length
* 11174 11273: gap of unknown length
* 11274 186485: contig of 175212 bp in length.
Location/Qualifiers
1. 186485
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-1026L22"
/clone_1fb="RP11-1026L22"
/clone_1fb="RP11-1026L22"

ORIGIN

Query Match 100.0%; Score 366; DB 2; Length 186485;
Best Local Similarity 100.0%; Freq. No. 6.7e-65;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCCTTAACCTGCTCTTCAAAAGTTGATAGTACAGTACAGTATTAATTAATTAATTTG 60
121990 CCCTTAACCTGCTCTTCAAAAGTTGATAGTACAGTACAGTATTAATTAATTTG 121931
61 GAAAAACAGCTCTGATATTTTCTGATGCTGATATATATATATTAATTAATTAATTTG 120
121930 GAAAAACAGCTCTGATATTTTCTGATGCTGATATATATATATTAATTAATTAATTTG 121871
121 AATCTATCTGATATTAAGTGTGACATCTTGACACCAATTTTAAGAAATAGCTGAG 180
121870 AATCTATCTGATATTAAGTGTGACATCTTGACACCAATTTTAAGAAATAGCTGAG 121811
181 ACCGATTAAGATATCCCTACCAAGTGAATAATTTGATGTTAAGAGGTACAGAT 240
121810 ACCGATTAAGATATCCCTACCAAGTGAATAATTTGATGTTAAGAGGTACAGAT 121751

241 TATCACTGATTTTGTCAGTTGCTTCCAAATGCTGTTGATTTCCCTCATTTGTTAAACAT 300
121750 TATCACTGATTTTGTCAGTTGCTTCCAAATGCTGTTGATTTCCCTCATTTGTTAAACAT 121691
301 TGACAGTATGTGACAAATGGAAAAAATCCAAATTAATTAAGTACATATTTGTTTC 360
121690 TGACAGTATGTGACAAATGGAAAAAATCCAAATTAATTAAGTACATATTTGTTTC 121631
361 AGCAAT 366
121630 AGCAAT 121625

RESULT 9

G07259 2580 bp DNA linear STS 19-OCF-1995
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 2580)
Hudson, T.
Whitehead Institute/MIT Center for Genome Research; Physically
Mapped ESTs
Unpublished (1995)

Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: GTGATTATGATAGCTTGGAATGG
Primer B: AATGGTCAACACTGCTGATCC
STS size: 121
PCR Profile:

Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:

Protocol:
Template: 10 ng
Primer: each 5 pm
dNTPs: each 4 mM
Tag Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3

FEATURES

Prepared with primer pairs derived from D43636 -- Unigene.
Location/Qualifiers
1. 2580
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="764_B_9; 792_D_7; 817_D_5; 882_B_5; 897_F_7;
946_E_4; 959_E_2; 738_F_11"
1871..1891
1871..1895
complement(1971..1991)

STS
primer_bind
primer_bind
complement(1971..1991)

Db
6 AGCATT 1

RESULT 12
AC106612/c
LOCUS
DEFINITION
AC106612 252055 bp DNA linear HTG 13-MAY-2003
Rattus norvegicus clone CH230-175A5, *** SEQUENCING IN PROGRESS
*** 6 unordered pieces.

AC106612
AC106612.5 GI:30579444
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
SOURCE
ORGANISM

REFERENCE
AUTHORS
1 (bases 1 to 252055)
Mizny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Albrooke, S., Amin, A., Angiano, D.,

Aryshebech, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandarsnake, D., Barber, M., Bernstein, M., Benahmed, F., Bismail, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Devila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dedier, D., Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Roches, S., Dunn, A., Durbin, K., Duval, B., Evans, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falle, T., Fan, G., Fernandez, S., Finley, M., Flegg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabis, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gboregeogys, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Gunstaine, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulik, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovac, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, D., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshuwa, L., Loulsged, H., Lozano, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E., McWhiney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Mlosovlevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Narkervic, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokeme, O., Okwum, G., Olariunassoon, A., Pal, S., Parks, K., Pestenak, S., Paul, H., Perez, A., Perez, L., Plankoch, C., Plopper, F., Polidexter, A., Popovic, D., Primus, E., Pu, L., L., Puzio, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Rial, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivera, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Severy, G., Scherer, S., Scott, G., Shaceman, S., Shen, H., Shetty, J., Shvertsdeyn, A., Sisson, I., Sitter, C. D., Smaiz, D., Sneed, A., Sodergren, E., Song, X. Z., Svatelle, R., Sosa, J., Steidle, M., Strong, R., Sutton, A., Swatek, A., Taber, Z., Umani, K., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, B., Umami, K., Valas, R., Vars, V., Villaseas, D., Waldron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlezyk, R., Woodson, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Zhou, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weisrock, G. and Gibbs, R. A.

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 252055)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:24819088.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine
Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GLRO
Center clone name: CH230-175A5

----- Summary Statistics

Assembly program: Atlas 3.0:
Consensus quality: 216498 bases at least Q40
Consensus quality: 220368 bases at least Q30
Consensus quality: 223168 bases at least Q20
Estimated insert size: 230938; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 243681: contig of 243681 bp in length
243782 243781: gap of unknown length
243782 244985: contig of 1204 bp in length
244985 245085: gap of unknown length
245085 246426: contig of 1341 bp in length
246426 246526: gap of unknown length
246526 247527: contig of 1001 bp in length
247527 247528: gap of unknown length
247528 248934: contig of 1307 bp in length
248934 249034: gap of unknown length
249034 252055: contig of 3021 bp in length.
Location/Qualifiers

FEATURES
source

misc_feature

misc_feature

1. 252055
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-175A5"
1303. 1905
/note="clone boundary
clone end:Sp6
site:EcoRI
end_sequence:BBH351404"
240925. 241490
/note="clone boundary
clone end:T7
site:EcoRI

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department


```

Db      42433 CCAGAGTTGATGTGCTGAGAACAACTTTCAGCT-AATTGTCAGATGCCCTTAG 42491
QY      270  TGTGTTGATTTCCCTCATTTGTAAACATTGACAGTATGTGACAAATGGAAAAA 329
Db      42492 TTCTGACCAAGCTTTTCTTGTGTGAACATTGACAGTATGTGACAGATGGAAATTA- 42550
QY      330  ATCCAATTAATAAGTGACATATTGTTGTTCCAGCAAT 366
Db      42551 --TCCAATTAATAAGTGACATATTGTTGTTCCAGCAAT 42585

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Search completed: January 31, 2005, 16:38:39
 Job time : 2043.02 secs

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Db 2050 TGAAGCTTTTCTTTAAGATCAGAAATGTAGCCAGTTCTTTGGCCAGAAGATGAATACT 2109
QY 181 TGAATATTTCTGAAAGGAGGGGTGAGATGGGTGTGGAGCATGTATAGTGTGATTTT 240
Db 2110 TGAATATTTCTGAAAGGAGGGGTGAGATGGGTGTGGAGCATGTATAGTGTGATTTT 2169
QY 241 ATTTCTTTCTTTGTGATGAGGGGCCAAGAGAAAGCATGAATCTTCCCTGTCAAGCTCT 300
Db 2170 ATTTCTTTCTTTGTGATGAGGGGCCAAGAGAAAGCATGAATCTTCCCTGTCAAGCTCT 2229
QY 301 TACAGCCACAGGACACTGTGTCTACTGTCTGGAAAGACATGTCCCCGTGGCTGTGGGCCCG 360
Db 2230 TACAGCCACAGGACACTGTGTCTACTGTCTGGAAAGACATGTCCCCGTGGCTGTGGGCCCG 2289
QY 361 TGGTCTGTTTAAATAAAGTGCGCTGG 388
Db 2290 TGGTCTGTTTAAATAAAGTGCGCTGG 2317

RESULT 2
BD272343 4186 bp DNA linear PAT 17-JUL-2003
LOCUS BD272343
DEFINITION Methods of diagnosing or treating neurological diseases and cell
degeneration.
ACCESSION BD272343.1 GI:33082111
VERSION BD272343.1
KEYWORDS JP 2002530076-A/3
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS 1 (bases 1 to 4186)
TITLE Nitach, R. and Greave, I.
METHODS Methods of diagnosing or treating neurological diseases and cell
degeneration
PATENT JP 2002530076-A 3 17-SEP-2002;
JOURNAL ROGER NITSCH, ISABELL GREVE
COMMENT OS Homo sapiens (human)
PN JP 2002530076-A/3
PD 17-SEP-2002 JP 2000582553
PF 12-NOV-1999 JP 2000582553
PR 12-NOV-1998 EP 98121478.6
PI ROGER NITSCH, ISABELL GREVE
PC C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00,
PC A61P1/00, A61P15/00, A61P21/00, A61P25/00, A61P25/14, A61P25/16,
PC A61P25/28,
PC A61P43/00, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, C12Q1/ PC
68, G01N33/53, G01N33/53, C12N15/00, C12N5/00, A61K37/02 CC Methods
of diagnosing or treating neurological diseases and CC
cell
FH CC degeneration
FT FT source
LOCATION/Qualifiers
1. .4186
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 388, DB 6, Length 4186,
Best Local Similarity 100.0%; Pred. No. 9, 2e-116;
Matches 388, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 TGTCCCTGGCCATCCATGTGATGTTTGGATGGAAGTTAACTTATGCCAGTGGGCACT 60
Db 3799 TGTCCCTGGCCATCCATGTGATGTTTGGATGGAAGTTAACTTATGCCAGTGGGCACT 3858

QY 61 GCATGTGAAGATCAGAGTAAGCTCTCCCTCCAGAGCCCTGATGTTCTTGGCTGCA 120
Db 3859 GCATGTGAAGATCAGAGTAAGCTCTCCCTCCAGAGCCCTGATGTTCTTGGCTGCA 3918
QY 121 TGAAGTTTTCTTTGAATCAGAAATTTGAGCCAGTTCTTTGGCCAGAAGATGAATACT 180
Db 3919 TGAAGTTTTCTTTGAATCAGAAATTTGAGCCAGTTCTTTGGCCAGAAGATGAATACT 3978
QY 181 TGAATATTTCTGAAAGGAGGGGTGAGATGGGTGTGGAGCATGTATAGTGTGATTTT 240
Db 3979 TGAATATTTCTGAAAGGAGGGGTGAGATGGGTGTGGAGCATGTATAGTGTGATTTT 4038
QY 241 ATTTCTTTCTTTGTGATGAGGGGCCAAGAGAAAGCATGAATCTTCCCTGTCAAGCTCT 300
Db 4039 ATTTCTTTCTTTGTGATGAGGGGCCAAGAGAAAGCATGAATCTTCCCTGTCAAGCTCT 4098
QY 301 TACAGCCACAGGACACTGTGTCTACTGTCTGGAAAGACATGTCCCCGTGGCTGTGGGCCCG 360
Db 4099 TACAGCCACAGGACACTGTGTCTACTGTCTGGAAAGACATGTCCCCGTGGCTGTGGGCCCG 4158
QY 361 TGGTCTGTTTAAATAAAGTGCGCTGG 388
Db 4159 TGGTCTGTTTAAATAAAGTGCGCTGG 4186

RESULT 3
AX026418 4186 bp DNA linear PAT 16-SEP-2000
LOCUS AX026418
DEFINITION Sequence 4 from Patent EP1002862.
ACCESSION AX026418
VERSION AX026418.1 GI:10187648
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS 1
TITLE Methods of diagnosing or treating neurological diseases
JOURNAL Patent: EP 1002862-A 4 24-MAY-2000;
NITSCH ROGER M PROF DR (DE)
COMMENT
LOCATION/Qualifiers
1. .4186
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 388, DB 6, Length 4186,
Best Local Similarity 100.0%; Pred. No. 9, 2e-116;
Matches 388, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 TGTCCCTGGCCATCCATGTGATGTTTGGATGGAAGTTAACTTATGCCAGTGGGCACT 60
Db 3799 TGTCCCTGGCCATCCATGTGATGTTTGGATGGAAGTTAACTTATGCCAGTGGGCACT 3858
QY 61 GCATGTGAAGATCAGAGTAAGCTCTCCCTCCAGAGCCCTGATGTTCTTGGCTGCA 120
Db 3859 GCATGTGAAGATCAGAGTAAGCTCTCCCTCCAGAGCCCTGATGTTCTTGGCTGCA 3918
QY 121 TGAAGTTTTCTTTGAATCAGAAATTTGAGCCAGTTCTTTGGCCAGAAGATGAATACT 180
Db 3919 TGAAGTTTTCTTTGAATCAGAAATTTGAGCCAGTTCTTTGGCCAGAAGATGAATACT 3978
QY 181 TGAATATTTCTGAAAGGAGGGGTGAGATGGGTGTGGAGCATGTATAGTGTGATTTT 240
Db 3979 TGAATATTTCTGAAAGGAGGGGTGAGATGGGTGTGGAGCATGTATAGTGTGATTTT 4038
QY 241 ATTTCTTTCTTTGTGATGAGGGGCCAAGAGAAAGCATGAATCTTCCCTGTCAAGCTCT 300
Db 4039 ATTTCTTTCTTTGTGATGAGGGGCCAAGAGAAAGCATGAATCTTCCCTGTCAAGCTCT 4098
QY 301 TACAGCCACAGGACACTGTGTCTACTGTCTGGAAAGACATGTCCCCGTGGCTGTGGGCCCG 360

Db 4099 TACGCCACAGGCACTGTCTACTGTCTGSAAGACATGTCCCTGCTGTGGGCGC 4158
Qy 361 TGCTTCTGTTTAATAAAGTGCCCTGG 388
Db 4159 TGCTTCTGTTTAATAAAGTGCCCTGG 4186

RESULT 4
BD272342 4187 bp DNA linear PAT 17-JUL-2003
LOCUS Methods of diagnosing or treating neurological diseases and cell
DEFINITION degeneration.
ACCESSION BD272342
VERSION BD272342.1 GI:33082110
KEYWORDS JP 2002530076-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 4187)
NITSCH, R. and Greeve, I.
TITLE Methods of diagnosing or treating neurological diseases and cell
degeneration
JOURNAL Patent: JP 2002530076-A 2 17-SEP-2002;
ROGER NITSCH, ISABELL GREVE
OS Homo sapiens (human)
PN JP 2002530076-A/2
PD 17-SEP-2002
PF 12-NOV-1999 JP 2000582553
PR 12-NOV-1998 EP 98121478.6
PI ROGER NITSCH, ISABELL GREVE
PC C12N15/09, A61K8/00, A61K39/395, A61K45/00, A61K48/00,
PC A61P11/00, A61P15/00, A61P21/00, A61P25/00, A61P25/14, A61P25/16,
PC A61P25/28,
PC A61P43/00, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, C12Q1/PC
68, G01N33/53, G01N33/53, C12N15/00, C12N5/00, A61K37/02 CC Methods
of diagnosing or treating neurological diseases and cell
degeneration
CC degeneration
FH key Location/Qualifiers
FT source 1. 4187
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

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Query Match 100.0%; Score 388; DB 6; Length 4187;
Best Local Similarity 100.0%; Pred. No. 9.2e-116; Indels 0; Gaps 0;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TGTCCTGGCCATCATGTGATGTTTGTGATGATTAACCTTATGCCAGTGGCAGT 60
Db 3800 TGTCCTGGCCATCATGTGATGTTTGTGATGATTAACCTTATGCCAGTGGCAGT 3859
Qy 61 GCATGTGAAAAGTATCAGATGAGCTCTCCCTCCAGAGCCCTGAGTTTCTGGCTGCA 120
Db 3860 GCATGTGAAAAGTATCAGATGAGCTCTCCCTCCAGAGCCCTGAGTTTCTGGCTGCA 3919
Qy 121 TGAAGTTTCTTTAGATCAGATTGATGACCACTTTCTTGGCAGAGGATGAATACT 180
Db 3920 TGAAGTTTCTTTAGATCAGATTGATGACCACTTTCTTGGCAGAGGATGAATACT 3979
Qy 181 TGAATATTACTGAAAGGAGGGGTGAGATGGGTGTGGCAGTGTATGTTGATTTT 240
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Qy 241 ATTTCTCTTTGGTCAATGGGGGCAAGSAGAAAGCATGATCTTCCCTGACGGCT 300
Db 4040 ATTTCTCTTTGGTCAATGGGGGCAAGSAGAAAGCATGATCTTCCCTGACGGCT 4099
Qy 301 TACAGCCACAGGCACTGTCTACTGTCTGGAAGACATGTCCCGTGGCTGTGGGCGC 360
Db 4100 TACAGCCACAGGCACTGTCTACTGTCTGGAAGACATGTCCCGTGGCTGTGGGCGC 4159
Qy 361 TGCTTCTGTTTAATAAAGTGCCCTGG 388
Db 4160 TGCTTCTGTTTAATAAAGTGCCCTGG 4187

RESULT 5
AX026417 4187 bp DNA linear PAT 16-SEP-2000
LOCUS Sequence 3 from Patent EP1002862.
ACCESSION AX026417
VERSION AX026417.1 GI:10187647
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
NITSCH, R. and Greeve, I.
TITLE Methods of diagnosing or treating neurological diseases
JOURNAL Patent: EP 1002862-A 3 24-MAY-2000;
NITSCH, R. and Greeve, I.
OS Homo sapiens (human)
PN EP 1002862-A 3
PD 17-SEP-2000
PF 12-NOV-1999 JP 2000582553
PR 12-NOV-1998 EP 98121478.6
PI ROGER NITSCH, ISABELL GREVE
PC C12N15/09, A61K8/00, A61K39/395, A61K45/00, A61K48/00,
PC A61P11/00, A61P15/00, A61P21/00, A61P25/00, A61P25/14, A61P25/16,
PC A61P25/28,
PC A61P43/00, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, C12Q1/PC
68, G01N33/53, G01N33/53, C12N15/00, C12N5/00, A61K37/02 CC Methods
of diagnosing or treating neurological diseases and cell
degeneration
CC degeneration
FH key Location/Qualifiers
FT source 1. 4187
/organism="Homo sapiens"
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ORIGIN
Query Match 100.0%; Score 388; DB 6; Length 4187;
Best Local Similarity 100.0%; Pred. No. 9.2e-116; Indels 0; Gaps 0;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TGTCCTGGCCATCATGTGATGTTTGTGATGATTAACCTTATGCCAGTGGCAGT 60
Db 3800 TGTCCTGGCCATCATGTGATGTTTGTGATGATTAACCTTATGCCAGTGGCAGT 3859
Qy 61 GCATGTGAAAAGTATCAGATGAGCTCTCCCTCCAGAGCCCTGAGTTTCTGGCTGCA 120
Db 3860 GCATGTGAAAAGTATCAGATGAGCTCTCCCTCCAGAGCCCTGAGTTTCTGGCTGCA 3919
Qy 121 TGAAGTTTCTTTAGATCAGATTGATGACCACTTTCTTGGCAGAGGATGAATACT 180
Db 3920 TGAAGTTTCTTTAGATCAGATTGATGACCACTTTCTTGGCAGAGGATGAATACT 3979
Qy 181 TGAATATTACTGAAAGGAGGGGTGAGATGGGTGTGGCAGTGTATGTTGATTTT 240
Db 3980 TGAATATTACTGAAAGGAGGGGTGAGATGGGTGTGGCAGTGTATGTTGATTTT 4039
Qy 241 ATTTCTCTTTGGTCAATGGGGGCAAGSAGAAAGCATGATCTTCCCTGACGGCT 300
Db 4040 ATTTCTCTTTGGTCAATGGGGGCAAGSAGAAAGCATGATCTTCCCTGACGGCT 4099
Qy 301 TACAGCCACAGGCACTGTCTACTGTCTGGAAGACATGTCCCGTGGCTGTGGGCGC 360
Db 4100 TACAGCCACAGGCACTGTCTACTGTCTGGAAGACATGTCCCGTGGCTGTGGGCGC 4159
Qy 361 TGCTTCTGTTTAATAAAGTGCCCTGG 388
Db 4160 TGCTTCTGTTTAATAAAGTGCCCTGG 4187

RESULT 6
AX334630 4187 bp DNA linear PAT 09-JAN-2002
LOCUS Sequence 5139 from Patent WO0194629.
DEFINITION

ACCESSION AX334630
VERSION AX334630.1 GI:18125349
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horizant, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
JOURNAL gene sets
Patent: WO 0194629-A 5139 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source 1. 4187
/organism="Homo sapiens"
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ORIGIN
Query Match 100.0%; Score 388; DB 6; Length 4187;
Best Local Similarity 100.0%; Pred. No. 9.2e-116;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTCCCTGGCCATCATGTGATGTTTGGATGAGTTAACTTGATGCGAGTGGCAGT 60
DB 3800 TGTCCCTGGCCATCATGTGATGTTTGGATGAGTTAACTTGATGCGAGTGGCAGT 3859
QY 61 GCATGTGAAAAGTATCAGAGTAAGCTCTCCCTCCAGAGCCCTGAGTTCTTGCTGCA 120
DB 3860 GCATGTGAAAAGTATCAGAGTAAGCTCTCCCTCCAGAGCCCTGAGTTCTTGCTGCA 3919
QY 121 TGAAGTTTCTTTAAGATCAGAAATTGAGCCAGTTCTTGCGCCAGAGAGTAATCT 180
DB 3920 TGAAGTTTCTTTAAGATCAGAAATTGAGCCAGTTCTTGCGCCAGAGAGTAATCT 3979
QY 181 TGGATATTAAGTGAAGGAGGAGTGAAGATGAGTGTGAGCATGTATGATGATTTT 240
DB 3980 TGGATATTAAGTGAAGGAGGAGTGAAGATGAGTGTGAGCATGTATGATGATTTT 4039
QY 241 ATTTTCTTTCTTTGTCATGAGGAGCCCAAGAGAAAGCATGATCTTCCCTGTCAGGCTCT 300
DB 4040 ATTTTCTTTCTTTGTCATGAGGAGCCCAAGAGAAAGCATGATCTTCCCTGTCAGGCTCT 4099
QY 301 TACAGCCACAGGACATGTCATCTCTGCGAAGATGTCCTCCCTGCTGAGGCGCC 360
DB 4100 TACAGCCACAGGACATGTCATCTCTGCGAAGATGTCCTCCCTGCTGAGGCGCC 4159
QY 361 TGCCTCTGTTTAATATAAGTGCCCTGG 388
DB 4160 TGCCTCTGTTTAATATAAGTGCCCTGG 4187
RESULT 7
AX408962 4187 bp DNA 1linear PAT 14-JUN-2002
LOCUS Sequence 1609 from Patent WO0229103.
DEFINITION AX408962
ACCESSION AX408962
VERSION AX408962.1 GI:21441667
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Alvarez, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G.
TITLE Gene expression profiles in liver cancer
JOURNAL Patent: WO 0229103-A 1609 11-APR-2002;
FEATURES
source 1. 4187
/organism="Homo sapiens"
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ORIGIN
Query Match 100.0%; Score 388; DB 6; Length 4187;
Best Local Similarity 100.0%; Pred. No. 9.2e-116;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTCCCTGGCCATCATGTGATGTTTGGATGAGTTAACTTGATGCGAGTGGCAGT 60
DB 3800 TGTCCCTGGCCATCATGTGATGTTTGGATGAGTTAACTTGATGCGAGTGGCAGT 3859
QY 61 GCATGTGAAAAGTATCAGAGTAAGCTCTCCCTCCAGAGCCCTGAGTTCTTGCTGCA 120
DB 3860 GCATGTGAAAAGTATCAGAGTAAGCTCTCCCTCCAGAGCCCTGAGTTCTTGCTGCA 3919
QY 121 TGAAGTTTCTTTAAGATCAGAAATTGAGCCAGTTCTTGCGCCAGAGAGTAATCT 180
DB 3920 TGAAGTTTCTTTAAGATCAGAAATTGAGCCAGTTCTTGCGCCAGAGAGTAATCT 3979
QY 181 TGGATATTAAGTGAAGGAGGAGTGAAGATGAGTGTGAGCATGTATGATGATTTT 240
DB 3980 TGGATATTAAGTGAAGGAGGAGTGAAGATGAGTGTGAGCATGTATGATGATTTT 4039
QY 241 ATTTTCTTTCTTTGTCATGAGGAGCCCAAGAGAAAGCATGATCTTCCCTGTCAGGCTCT 300
DB 4040 ATTTTCTTTCTTTGTCATGAGGAGCCCAAGAGAAAGCATGATCTTCCCTGTCAGGCTCT 4099
QY 301 TACAGCCACAGGACATGTCATCTCTGCGAAGATGTCCTCCCTGCTGAGGCGCC 360
DB 4100 TACAGCCACAGGACATGTCATCTCTGCGAAGATGTCCTCCCTGCTGAGGCGCC 4159
QY 361 TGCCTCTGTTTAATATAAGTGCCCTGG 388
DB 4160 TGCCTCTGTTTAATATAAGTGCCCTGG 4187
RESULT 8
AX828407 4187 bp DNA 1linear PAT 12-DEC-2003
LOCUS Sequence 53 from Patent WO03074073.
DEFINITION AX828407
ACCESSION AX828407
VERSION AX828407.1 GI:39838407
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Al-Mahmoud, S., Colin, S. and Schneider, C.
TITLE Genes involved in regulating angiogenesis, pharmaceutical
JOURNAL preparations containing same and applications thereof
Patent: WO 03074073-A 53 12-SEP-2003;
FEATURES
source 1. 4187
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9.2e-116;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTCCCTGGCCATCATGTGATGTTTGGATGAGTTAACTTGATGCGAGTGGCAGT 60
DB 3800 TGTCCCTGGCCATCATGTGATGTTTGGATGAGTTAACTTGATGCGAGTGGCAGT 3859
QY 61 GCATGTGAAAAGTATCAGAGTAAGCTCTCCCTCCAGAGCCCTGAGTTCTTGCTGCA 120
DB 3860 GCATGTGAAAAGTATCAGAGTAAGCTCTCCCTCCAGAGCCCTGAGTTCTTGCTGCA 3919

QY	121	GAAGGCTTTCTTTGAATTCAGAAATTGATAGCAGGTTCTTTGGCCAGAAAGATGAATCT	180
Db	3920	TGAAGCTTTCTTTTGAATTCAGAAATTGATAGCAGGTTCTTTGGCCAGAAAGATGAATCT	3979
QY	181	TGATATATTACTGAAAAGGAGGGGTGAGATGGGTGTGGCAGTGTATGGTGTGTGATTTTT	240
Db	3980	TGATATATTACTGAAAAGGAGGGGTGAGATGGGTGTGGCAGTGTATGGTGTGTGATTTTT	4039
QY	241	ATTTTCTTCTTTTGGTCATGGGGGGCCAGAGAGAAAGCATGAAATCTTCCCTGTCAAGCTCT	300
Db	4040	ATTTTCTTCTTTTGGTCATGGGGGGCCAGAGAGAAAGCATGAAATCTTCCCTGTCAAGCTCT	4099
QY	301	TACAGCCACAGGCACTGTGTCTACTGTGTGAAAGCATGTCCCGTGGCTGTGGGGCCGC	360
Db	4100	TACAGCCACAGGCACTGTGTCTACTGTGTGAAAGCATGTCCCGTGGCTGTGGGGCCGC	4158
QY	361	TGCTTCTGTTTAAATPAAAGTGCCCTGG	388
Db	4160	TGCTTCTGTTTAAATPAAAGTGCCCTGG	4187
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LOCUS	HUMRSC390	4187 bp	mRNA linear PRI 06-OCT-2001
DEFINITION	Human sapiens mRNA for KIAA0018 protein, partial cds.		
ACCESSION	D13643		
VERSION	D13643.2	GI:6630631	
KEYWORDS	KIAA0018 protein.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S.		
TITLE	Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1		
JOURNAL	DNAREG	1 (1), 27-35 (1994)	
MEDLINE	96051387		
PUBMED	7584026		
REFERENCE	2		
AUTHORS	Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S.		
TITLE	Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)		
JOURNAL	DNAREG	1 (1), 47-56 (1994)	
MEDLINE	96051389		
PUBMED	7584028		
REFERENCE	3 (bases 1 to 4187)		
AUTHORS	Ohara, O., Nagase, T., Kikuno, R. and Nomura, N.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-NOV-1992)	Osamu Ohara, Kazuo DNA Research Institute, 152-3, Yana, Kisarazu, Chiba 292-0612, Japan	
COMMENT	(E-mail: chnainfo@kazuo.or.jp, Tel: +81-438-52-3913)		
FEATURES	On Dec 22, 1999 this sequence version replaced gi:285996.		
SOURCE	Sequence updated (20-Dec-1999).		
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	61	GCATGTGGAAAGTATCAGAGTAACTTCCCTCCAGAGCCCTGAGTTTCTGGCTGCA	120			
	3860	GCATGTGGAAAGTATCAGAGTAACTTCCCTCCAGAGCCCTGAGTTTCTGGCTGCA	3919			
	121	TGAAGTTTCTTTAGATCAGAAATGAGCAGTTCTTTGGCCAGAGGATGAATACT	180			
	3920	TGAAGTTTCTTTAGATCAGAAATGAGCAGTTCTTTGGCCAGAGGATGAATACT	3979			
	181	TGATATTACTGAAAGGAGGAGTGAAGATGGTGTGGCAGTGTATGGTGTGATTTT	240			
	3980	TGATATTACTGAAAGGAGGAGTGAAGATGGTGTGGCAGTGTATGGTGTGATTTT	4039			
	241	ATTTTCTTTTGGTCAATGGGGGCGAAGAGAAAGCATGATCTTCCCTGCAGCTCT	300			
	4040	ATTTTCTTTTGGTCAATGGGGGCGAAGAGAAAGCATGATCTTCCCTGCAGCTCT	4099			
	301	TACAGCCACAGGCACTGTCTACTGTCTGGAACAATGTCCCGTGGCTGTGGGGCGC	360			
	4100	TACAGCCACAGGCACTGTCTACTGTCTGGAACAATGTCCCGTGGCTGTGGGGCGC	4159			
	361	TGCTCTGTTTAATAAAGAGGCGCTG 388				
	4160	TGCTCTGTTTAATAAAGAGGCGCTG 4187				
RESULT 10	BC004375	4202 bp	mRNA	linear	PRI 29-JUN-2004	
LOCUS	BC004375					
DEFINITION	Homo sapiens 24-dehydrocholesterol reductase, mRNA (cDNA clone					
ACCESSION	BC004375					
VERSION	BC004375.1					
KEYWORDS	MG.					
SOURCE	Homo sapiens (human)					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1 (bases 1 to 4202)					
	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, G.,					
	Klauser, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,					
	Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,					
	Hopkins, R.F., Jordan, H., Moore, T., Max, S.T., Wang, J., Heien, F.,					
	Diatcenco, L., Marusina, K., Palmer, A.A., Rubin, G.M., Hong, L.,					

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
JOURNAL

REMARK

COMMENT

FEATURES

source

gene

CDS

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loguella, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McKernan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richard, S., Wierley, R.C., Hale, S., Garcia, A.M., Gay, L.J., Hui, X., Gibbs, R.A., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.S., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 4202)
Strausberg, R.
Direct Submission
Submitted (12-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Ohi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lila Prabhu, Parvaneh Saeedi, JR Santos, Angeliq Scherch, Ursula Skalska, Duane Smalins, Jeff Stott, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAL Plate: 13 Row: f Column: 10.
Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 388; Da 9; Length 4202;
Best Local Similarity 100.0%; Pred. No. 9, 2e-116;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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121 TGAAGGTTTCTTTAGAAATCAGAAATTTAGCCAGTTCTTTGGCCAGAGATGATACT 180
3917 TGAAGGTTTCTTTAGAAATCAGAAATTTAGCCAGTTCTTTGGCCAGAGATGATACT 3976
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4097 TACAGCAGCAGCAGCTGCTGCTACTGCTGGAAGACATGCTCCGCTGCTGAGGCGCG 4156
361 TCGTTCTGTTTAATAATAAAGTGGCTGG 388
4157 TCGTTCTGTTTAATAATAAAGTGGCTGG 4184

RESULT 11

BD272341

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BD272341 4248 bp DNA linear PAT 17-UTL-2003
Methods of diagnosing or treating neurological diseases and cell degeneration.
BD272341
BD272341.1 GI:33082109
JP 2002530076-A/1.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 4248)
Nitsch, R. and Greve, I.
Methods of diagnosing or treating neurological diseases and cell degeneration
Patent: JP 2002530076-A 1 17-SEP-2002;
ROGER NITSCH, ISABELL GREVE
OS Homo sapiens (human)
PN JP 2002530076-A/1
PN 17-SEP-2002
PR 12-NOV-1999 JP 2000582553
PR 12-NOV-1998 EP 98121478.6
PI ROGER NITSCH, ISABELL GREVE
PC C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00, A61P1/00,
PC A61P11/00, A61P15/00, A61P21/00, A61P25/00, A61P25/14, A61P25/16,
PC A61P25/28,
PC A6143/00, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, C12O1/ PC
68, G01N33/53, G01N33/53, C12N15/00, C12N5/00, A61K37/02 CC Methods
of diagnosing or treating neurological diseases and CC

cell degeneration
CC key Location/Qualifiers
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FT /organism="Homo sapiens (human)"

FEATURES
source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 9.2e-116; Mismatches 0; Indels 0; Gaps 0;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3921 GCATGTGAAAAGTATCAGATTAAGCTCTCCCTCCAGAGCCCTGAGTTTCTTGGCTGCA 3980

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QY 181 TGAATATTACTGAAAAGGAGGAGTGAAGATGGGTGTGAGATGCTATGATGATTTT 240
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QY 241 ATTTTCTTCTTTGGTCAATGGGGCCAAAGAGAAAGCATGATTTCCCTGACGCTCT 300
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DB 4161 TACAGCCACAGGACCTGTCTACTGTCTGGAAGACATGTCGCCGTGGGGCCGC 4220

QY 361 TGCTTCGTTTAAATAAAGTGCCCTGG 388
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LOCUS Sequence 329 from Patent EP1394274.
DEFINITION CQ776643
ACCESSION CQ776643
VERSION CQ776643.1 GI:45380033
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuahara,K.
METHODS of testing for bronchial asthma or chronic obstructive
pulmonary disease
Patent: EP 1394274-A 329 03-MAR-2004;
JOURNAL Genex Research, Inc. (JP)
TITLE Location/Qualifiers
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QY 361 TGCTTCGTTTAAATAAAGTGCCCTGG 388
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LOCUS Sequence 526 from Patent EP1394274.
DEFINITION CQ776840
ACCESSION CQ776840
VERSION CQ776840.1 GI:45380230
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuahara,K.
METHODS of testing for bronchial asthma or chronic obstructive
pulmonary disease
Patent: EP 1394274-A 526 03-MAR-2004;
JOURNAL Genex Research, Inc. (JP)
TITLE Location/Qualifiers
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source 1..4248
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RESULT 14
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LOCUS Sequence 2 from Patent EP1002862.
ACCESSION AX026416
VERSION AX026416.1 GI:10187646
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Methods of diagnosing or treating neurological diseases
AUTHORS Patent: EP 1002862-A 2 24-MAY-2000;
JOURNAL NITSCH ROGER M PROF DR (DE)
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/db_xref="taxon:9606"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9.2e-116;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 3921 GCATGTGAAAGATACAGATAGCCTCCCTCCAGAGCCCTGAGTTCTTGGCTGCA 3980
QY 121 TGAAGGTTTCTTTAGATCAGATTGTAGCCAGTTCTTGGCCAGAGATGAATACT 180
DB 3981 TGAAGGTTTCTTTAGATCAGATTGTAGCCAGTTCTTGGCCAGAGATGAATACT 4040
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QY 301 TACAGCCACAGGACGCTGTCTACTGTCTGTGGAAGACATGTCCTCCCGTGTGGGGCCGC 360
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RESULT 15
AX828386 4248 bp DNA linear PAT 12-DEC-2003
LOCUS Sequence 32 from Patent WO03074073.
DEFINITION

ACCESSION AX828386
VERSION AX828386.1 GI:39838386
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Al-Mahmoud, S., Colin, S. and Schneider, C.
AUTHORS Genes involved in regulating angiogenesis, pharmaceutical
TITLES preparations containing same and applications thereof
JOURNAL Patent: WO 03074073-A 32 12-SEP-2003;
Gene Signal (PR)
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source 1. 4248
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Best Local Similarity 100.0%; Pred. No. 9.2e-116;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTCCCTGGCCATCCATGTCATGATGTTGGATGAGTTAACTTGATGCCAGTGGGCACT 60
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QY 121 TGAAGGTTTCTTTAGATCAGATTGTAGCCAGTTCTTGGCCAGAGATGAATACT 180
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QY 301 TACAGCCACAGGACGCTGTCTACTGTCTGTGGAAGACATGTCCTCCCGTGTGGGGCCGC 360
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Search completed: January 31, 2005, 16:38:28
Job time : 2162.47 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

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Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	400	100.0	4187	6	AX334630
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7	400	100.0	4187	6	AX828407
8	400	100.0	4187	9	HUMRSC390
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11	400	100.0	4248	6	CQ776840
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13	400	100.0	4248	6	AX828386
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23	331	82.8	1594	10	AY039762	AY039762 Mus muscu
24	323	80.8	3836	6	BD235746	BD235746 Hypoxia r
25	322	80.5	1557	6	AX814446	AX814446 Sequence
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31	272.8	68.2	169072	9	AC009946	AC009946 Homo sapi
32	224.6	56.1	3994	10	BX11043	BX11043 Mouse DNA
33	224.6	56.1	246011	10	AL929585	AL929585 Mouse DNA
34	215	53.8	21500	2	AC117905	AC117905 Rattus no
35	215	53.8	262897	2	AC129688	AC129688 Rattus no
36	168.8	42.2	2012	5	BC078029	BC078029 Xenopus 1
37	167.2	41.8	1994	5	BC074393	BC074393 Xenopus 1
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39	109.2	27.3	154067	2	BX649302	BX649302 Dario rer
40	109.2	27.3	180994	5	BX255909	BX255909 Zebrafish
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ALIGNMENTS

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LOCUS
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Methods of diagnosing or treating neurological diseases and cell degeneration.
ACCESSION
BD272343.1 GI:33082111
VERSION
JP 2002530076-A/3.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 4186)
Nitsch,R., and Greeve,I.
METHODS OF DIAGNOSING OR CREATING NEUROLOGICAL DISEASES AND CELL DEGENERATION
Patent: JP 2002530076-A 3 17-SEP-2002;
JOURNAL
ROGER NITSCH, ISABELL GREVE
COMMENT
OS Homo sapiens (human)
PN JP 2002530076-A/3
PD 17-SEP-2002
PR 12-NOV-1999 JP 2000582553
PR 12-NOV-1998 EP 98121478.6
PI ROGER NITSCH, ISABELL GREVE
PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61K48/00,
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PC G01N33/53,G01N33/53,C12N15/00,C12N5/00,A61K37/02 CC Methods
of diagnosing or treating neurological diseases and cell
degeneration
CC
FH Key location/Qualifiers
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LOCUS	AX026418	4186 bp	DNA
DEFINITION	Sequence 4 from Patent EP1002862.		linear
			PAT 16-SEP-2000

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
1		Methods of diagnosing or treating neurological diseases		
		Patent: EP 1002862-A 4 24-MAY-2000;		
	NITSCH ROGER M PROF DR-UBI			
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Db	301	CGTTCAATGTGCACGGGGCGCGCTGGCTGGCTCACTGTCTTCATCTAAGTGTGGGAAGTACA	360
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DEFINITION	BD272342 4187 bp DNA linear PAT 17-JUL-2003 Methods of diagnosing or treating neurological diseases and cell degeneration.
ACCESSION	BD272342
VERSION	BD272342.1 GI:33082110
KEYWORDS	UP 2002530076-R/2.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 4187) Nitsch,R.,and Greeve,I. Methods of diagnosing or treating neurological diseases and cell
AUTHORS	
TITLE	

TITLE	JOURNAL	COMMENT
Methods of diagnosing or treating neurological diseases and cell degeneration	Patent: JP 2002530076-A 2 17-SEP-2002;	
	ROGER NITSCH, ISABELL GREEVE	
	Os Homo sapiens (human)	
	PN JP 2002530076-A/2	
	PD 17-SEP-2002	
	PP 12-NOV-1999 JP 2000582553	
	PR 12-NOV-1998 EP 98121478, 6	
	PI ROGER NITSCH, ISABELL GREEVE	
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Matches 400; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 GGGGCGAAGCCGAGGCGTTACCGCGCGGCGCGACACATGAGAGCCGCGCTGTGCTGG 60
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 Db 1 GGGGCGAAGCCGAGGCGTTACCGCGCGGCGCGACACATGAGAGCCGCGCTGTGCTGG 60
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 QY 61 CCGCTGTCGCGCGCTCTTCCTGCTGCGGTGCGCCGTAAGGGGCTGGAATTGCTGCTCA 120

Db	61	CCGCTGCGCGCTCTCTTCTGCTGTGGGTGGCCCTGAGGGCTGAGTTGCTGCTCA	120
Qy	121	TCACACAGCGCTGGGGTGTTCGTGTGCTCTTCTCTGCGGCTCTCGCTTATCTTCGATA	180
Db	121	TCACACAGCGCTGGGGTGTTCGTGTGCTCTTCTCTGCGGCTCTCGCTTATCTTCGATA	180
Qy	181	TCTACTACTAGTGTGCGCGCTGGGTGTGTTCAGAGCTTCAGAGGCTTCGGCTTGACAG	240
Db	181	TCTACTACTAGTGTGCGCGCTGGGTGTGTTCAGAGCTTCAGAGGCTTCGGCTTGACAG	240
Qy	241	AGCAGCGGCTGCGGACATTCAGAAAGAGTGGCGGAAATGGAAAGAGAGGGATGACAGA	300
Db	241	AGCAGCGGCTGCGGACATTCAGAAAGAGTGGCGGAAATGGAAAGAGAGGGATGACAGA	300
Qy	301	CCTTCATGTGACGGGGGCGCCCTGGCTGGACTCACTGTCTCACTACGTGTGGGAAATCA	360
Db	301	CCTTCATGTGACGGGGGCGCCCTGGCTGGACTCACTGTCTCACTACGTGTGGGAAATCA	360
Qy	361	AGAAACACACAAACATCATATCAACTGATGAGACAT	400
Db	361	AGAAACACACAAACATCATATCAACTGATGAGACAT	400
RESULT 4			
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LOCUS	AX026417	4187 bp	DNA
DEFINITION	Sequence 3 from Patent Epi1002862.		linear
ACCESSION	AX026417		
VERSION	AX026417.1	GI:10187647	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1		
AUTHORS			
TITLE	Methods of diagnosing or treating neurological diseases		
JOURNAL	Patent: EP 1002862-A 3 24-MAY-2000;		
	NITSCH ROGER M PROF DR (DE)		
FEATURES			
source	Location/Qualifiers		
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	/db_xref="taxon:9606"		
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Query Match	100.0%; Score 400; DB 6;	Length 4187;	
Best Local Similarity	100.0%; Pred. No. 1,86-67;		
Matches	400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	GGCGGAACCGCAGCGCTTACCGCGCGGCGCGACACCATGAGCCCGCTGTGCTGG	60
Db	1	GGCGGAACCGCAGCGCTTACCGCGCGGCGCGACACCATGAGCCCGCTGTGCTGG	60
Qy	61	CGGTGTGCGCTGCTCTTCTGCTGTGGTGCCTGAGGGGCTGAGGTTGCTGCTCA	120
Db	61	CGGTGTGCGCTGCTCTTCTGCTGTGGTGCCTGAGGGGCTGAGGTTGCTGCTCA	120
Qy	121	TTCACAGCGCTGGGTGTTCGTGTGCTCTTCTCTGCGCTCTCGCTTATCTTCGATA	180
Db	121	TTCACAGCGCTGGGTGTTCGTGTGCTCTTCTCTGCGCTCTCGCTTATCTTCGATA	180
Qy	181	TCTACTACTAGTGTGCGCGCTGGGTGTGTTCAGAGCTTCAGAGGCTTCGGCTTGACAG	240
Db	181	TCTACTACTAGTGTGCGCGCTGGGTGTGTTCAGAGCTTCAGAGGCTTCGGCTTGACAG	240
Qy	241	AGCAGCGGCTGCGGACATTCAGAAAGAGTGGCGGAAATGGAAAGAGAGGGATGACAGA	300
Db	241	AGCAGCGGCTGCGGACATTCAGAAAGAGTGGCGGAAATGGAAAGAGAGGGATGACAGA	300
Qy	301	CCTTCATGTGACGGGGGCGCCCTGGCTGGACTCACTGTCTCACTACGTGTGGGAAATCA	360
Db	301	CCTTCATGTGACGGGGGCGCCCTGGCTGGACTCACTGTCTCACTACGTGTGGGAAATCA	360

Dd		301 CCTTCATGTGACGGGGCGCCCTTGCTGGTCTCACTGCTCATTACAGCTGTGGGAATACA	360
Oy		361 AGAAGACACAAAAACATCATGTATCAACTGATGCAT	400
Dd		361 AGAAGACACAAAAACATCATGTATCAACTGATGCAT	400
RESULT 5			
AXJ34630			
LOCUS	AXJ34630	4187 bp	DNA
DEFINITION	Sequence 5139 from Patent WO0194629.		linear
ACCESSION	AXJ34630		PAT 09-JAN-2002
VERSION	AXJ34630.1	GI:18125349	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
AUTHORS	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.		
REFERENCE	1 Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G., Horrigan,S., Soppel,D.R. and Weaver,Z. Cancer gene determination and therapeutic screening using signature gene sets Patent: WO 0194629-A 5139 13-DEC-2001; Avalon Pharmaceuticals (US) Location/Qualifiers 1..4187 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"		
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Matches 400;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
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Dd		1 GGCGCGAACCGCGACGCTTAACCGCGGGGCCGACAAATGAGCCCGCGTGCCTGG	60
Oy		61 CCGTGTGCGCGCTCTCTTCTCGTGTGGGNGCGCTGMAAGGGCGCTGAGTTGCTGTCA	120
Dd		61 CCGTGTGCGCGCTCTCTTCTCGTGTGGGNGCGCTGMAAGGGCGCTGAGTTGCTGTCA	120
Oy		121 TCACCAAGCGCTGGGGTGTGCTGTGCTCTTCTCTCGCGCGCTGCGCTTATCTTGATA	180
Dd		121 TCACCAAGCGCTGGGGTGTGCTGTGCTCTTCTCTCGCGCGCTGCGCTTATCTTGATA	180
Oy		181 TCTACTACTAAGTGCAGCGCGCTGGTGGTTCMAAGCTCAGAGAAGGCTCCGCGCTTGACG	240
Dd		181 TCTACTACTAAGTGCAGCGCGCTGGTGGTTCMAAGCTCAGAGAAGGCTCCGCGCTTGACG	240
Oy		241 AGCAGCGCGTGCAGGACATCCAGAAAGAGGTGCGGAATGGAAAGAGCAGGGTAGCAAGA	300
Dd		241 AGCAGCGCGTGCAGGACATCCAGAAAGAGGTGCGGAATGGAAAGAGCAGGGTAGCAAGA	300
Oy		301 CCTTCATGTGACGGGGCGCCCTTGCTGGTCACTGTCTCACTACGTGTGGGAATACA	360
Dd		301 CCTTCATGTGACGGGGCGCCCTTGCTGGTCACTGTCTCACTACGTGTGGGAATACA	360
Oy		361 AGAAGACACAAAAACATCATGTATCAACTGATGCAT	400
Dd		361 AGAAGACACAAAAACATCATGTATCAACTGATGCAT	400
RESULT 6			
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LOCUS	AX408962	4187 bp	DNA
DEFINITION	Sequence 1609 from Patent WO0229103.		linear
ACCESSION	AX408962		PAT 14-JUN-2002
VERSION	AX408962.1	GI:21441667	
KEYWORDS			
SOURCE	Homo sapiens (human)		

ORGANISM	Homio sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 Alvaras, C., Horne, D., Peres-da-Silva, S. and Vockley, J. G.
JOURNAL	Gene expression profiles in liver cancer Patent: WO 0229103-A 1609 11-APR-2002; GENE LOGIC INC (US)
FEATURES	Location/Qualifiers
source	1. 4187 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" /note="EMBL/GenBank Accession No. D13643"
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Query Match	100.0%; Score 400; DB 6; Length 4187;
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QY	1 GGGGGGAACCCGACCGCTTACCGGGGGGGCCGACCATGAGACCCCGCTGTGCTGG 60
DB	1 GGGGGGAACCCGACCGCTTACCGGGGGGGCCGACCATGAGACCCCGCTGTGCTGG 60
QY	61 CCGTGTGGCGCGCTGCTTCTCGTGTGGGATCGCCTGAAGGGGCTGAGATTGCTCA 120
DB	61 CCGTGTGGCGCGCTGCTTCTCGTGTGGGATCGCCTGAAGGGGCTGAGATTGCTCA 120
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DB	121 TCACCAAGGCTGGGATGTTGTTGTTGTTGTCCTTCTCTGCGGCTCGCTTATCTTGATA 180
QY	181 TCTACTACTAGCTGGCGGCTGGGTGTGTTCAACTGACGAGCGCTCGCGCTTGACG 240
DB	181 TCTACTACTAGCTGGCGGCTGGGTGTGTTCAACTGACGAGCGCTCGCGCTTGACG 240
QY	241 AGCAGCGCGTGGGGACATCCAGAAAGCAGATCGGGAAATGAAAGAGCAGGTACAGA 300
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QY	301 CCTTCATGTGCAAGCGGGCGCCCTGGCTGGCTCACTGTCTCACTACGTGTGGGAAGTACA 360
DB	301 CCTTCATGTGCAAGCGGGCGCCCTGGCTGGCTCACTGTCTCACTACGTGTGGGAAGTACA 360
QY	361 AGAAGACACACAAAACATCATGATCAACCTGATGAGATC 400
DB	361 AGAAGACACACAAAACATCATGATCAACCTGATGAGATC 400
RESULT 7	
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LOCUS	AX828407
DEFINITION	Sequence 53 from Patent WO03074073.
ACCESSION	AX828407
VERSION	AX828407.1 GI:39838407
KEYWORDS	
SOURCE	
ORGANISM	Homio sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 Al-Mahmoud, S., Colin, S. and Schneider, C.
JOURNAL	Genes involved in regulating angiogenesis, pharmaceutical preparations containing same and applications thereof Patent: WO 03074073-A 53 12-SEP-2003; Gene Signal (FR)
FEATURES	Location/Qualifiers
source	1. 4187 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"

Query Match	100.0%	Score 400	DB 6	Length 4187
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QY	1	GGCGGGAACCCGCGACCGCTTACCGCGCGCGCGCGACCATGAGCCCGCGGTGCTGG	60	
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QY	61	CCGTGTGCGGCGTGTCTTTCTTCTGTGTGGGTGGGCGCTGAAGGGGCTGGAGTTGCTCTCA	120	
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QY	121	TCACCGAGCGCTGGGGTGTGTGTGCTCTTCCCTCCGCGCGCTGTGCTTATCTTGGATA	180	
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QY	181	TCTACTACTACGTCGCGCGCTGGGTGGTGTTCATGACTCAGCAGCGCTCCGCGCTGCACG	240	
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QY	241	AGCAGCGCGGTGGCGGACATCAGAGCAGGTGGCGGATGGAGAGCAGCGGTATGCACAGA	300	
Db	241	AGCAGCGCGGTGGCGGACATCAGAGCAGGTGGCGGATGGAGAGCAGCGGTATGCACAGA	300	
QY	301	CCCTTCATGTGACAGGGGCGCGCTGGCGGTGCTCACTGTCTACTACGTTGTGGGGAAGTACA	360	
Db	301	CCCTTCATGTGACAGGGGCGCGCTGGCGGTGCTCACTGTCTACTACGTTGTGGGGAAGTACA	360	
QY	361	AGAAGACACACAAAACATCATGTATCAACCTGATGGACAT	400	
Db	361	AGAAGACACACAAAACATCATGTATCAACCTGATGGACAT	400	
RESULT 8				
HUMRSC390		4187 bp	mRNA	linear
LOCUS				PRI 06-OCT-2001
ACCESSION				
DEFINITION				Homo sapiens mRNA for KIAA0018 protein, partial cds.
VERSION				D13643
KEYWORDS				D13643.2 GI:6630631
SOURCE				KIAA0018 protein.
ORGANISM				Homo sapiens (human)
REFERENCE				Homo sapiens
AUTHORS				Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE				1
				Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S.
				Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1
				2
				Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S.
				Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)
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				Sequence updated (20-dec-1999).
				Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 1.8e-67;
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QY 1 GGGCGGAACCCGCGGCTTACCGCGGGCGCCGACCATGAGACCCCGCTGCTGG 60
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BD272341 4248 bp DNA linear PAT 17-JUL-2003
LOCUS BD272341
DEFINITION Methods of diagnosing or treating neurological diseases and cell degeneration.
ACCESSION BD272341
VERSION BD272341.1 GI:33082109

KEYWORDS JP 2002530076-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 4248)
AUTHORS Nitsch, R. and Greeve, I.
TITLE Methods of diagnosing or treating neurological diseases and cell degeneration
JOURNAL Patent: JP 2002530076-A 1 17-SEP-2002;
ROGER NITSCH, ISABELL GREEVE
COMMENT OS Homo sapiens (human)
PN JP 2002530076-A/1
PD 17-SEP-2002 JP 200058253
PF 12-NOV-1999 JP 200058253
PR 12-NOV-1998 EP 98121478.6
PI ROGER NITSCH, ISABELL GREEVE
PC C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00, A61P1/00, A61P11/00, A61P15/00, A61P21/00, A61P25/00, A61P25/14, A61P25/16, A61P25/28,
PC A61P43/00, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, C12Q1/PC 68,
PC G01N33/53, G01N33/53, C12N15/00, C12N5/00, A61K37/02 CC Methods of diagnosing or treating neurological diseases and CC
cell degeneration
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Best Local Similarity 100.0%; Pred. No. 1.7e-67;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 10
C0776643

LOCUS CO076643 4248 bp DNA linear PAT 11-MAR-2004
DEFINITION Sequence 329 from Patent EP1394274.
ACCESSION CO076643
VERSION CO076643.1 GI:45380033
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Ohtani, N., Sugita, Y., Yamaya, M., Kubo, H., Nagai, H. and Izuhara, K.
TITLE Methods of testing for bronchial asthma or chronic obstructive
pulmonary disease
JOURNAL Patent: EP 1394274-A 329 03-MAR-2004;
Genex Research, Inc. (JP)
FEATURES
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Query Match 100.0%; Score 400; DB 6; Length 4248;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCGGAAACCCGAGCGCTTACCGCGCGCGCGCACATGAGCCCGCGTGCCTGG 60
DB 62 GGGCGGAAACCCGAGCGCTTACCGCGCGCGCGCACATGAGCCCGCGTGCCTGG 121
QY 61 CCGTGTGCGCGCTGCTCTTCTCTGCTGTGGTGGCTGGAAGGGAGTTCGTCTCA 120
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DEFINITION Sequence 526 from Patent EP1394274.
ACCESSION CO076840
VERSION CO076840.1 GI:45380230
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Ohtani, N., Sugita, Y., Yamaya, M., Kubo, H., Nagai, H. and Izuhara, K.
TITLE Methods of testing for bronchial asthma or chronic obstructive
pulmonary disease
JOURNAL Patent: EP 1394274-A 526 03-MAR-2004;
Genex Research, Inc. (JP)
FEATURES
Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 1.7e-67;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCGGAAACCCGAGCGCTTACCGCGCGCGCGCACATGAGCCCGCGTGCCTGG 60
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DB 422 AGAAGACACACAAAACATCATGATCAACCTGATGACAT 461
RESULT 12
LOCUS AX026416 4248 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 2 from Patent EP1002862.
ACCESSION AX026416
VERSION AX026416.1 GI:10187646
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS NITSCH ROGER M PROF DR (DE)
TITLE Methods of diagnosing or treating neurological diseases
JOURNAL Patent: EP 1002862-A 2 24-MAY-2000;
NITSCH ROGER M PROF DR (DE)
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QY 301 CCTTCATGTGACGGGGGCGCGCTGCTGCTCACTACGTCTCACTACGTCTGCGGAAGTACA 360
DB 422 AGAAGACACACAAAACATCATGATCAACCTGATGACAT 461
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AX828386 4248 bp DNA linear PAT 12-DEC-2003
LOCUS Sequence 32 from Patent WO03074073.
DEFINITION AX828386
VERSION AX828386.1 GI:39838386
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Al-Mahmoud, S., Colin, S. and Schneider, C.
TITLE Genes involved in regulating angiogenesis, pharmaceutical preparations containing same and applications thereof
JOURNAL Patent: WO 03074073-A 32 12-SEP-2003;
Gene Signal (FR)
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ACCESSION AF261758
VERSION AF261758.1 GI:10442024
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Greave, I., Hermans-Borgmeyer, I., Brellinger, C., Kasper, D.,
TITLE The human DIMINUTO/DWARF1 homolog beladin-1 confers resistance to Alzheimer's disease-associated neurodegeneration and oxidative stress
JOURNAL J. Neurosci. 20 (19), 7345-7352 (2000)
MEDLINE 20482303
PUBMED 11007892
REFERENCE 2 (bases 1 to 4248)
AUTHORS Greave, I.
TITLE Direct Submission
JOURNAL Submitted (28-APR-2000) Center for Molecular Neurobiology, Martinistrasse 52, Hamburg 20246, Germany
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 ACCESSION BC011669
 VERSION
 KEYWORDS
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 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 4254)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marsina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, D., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S.,
 Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
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 Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bontfard, G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E.,
 Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 JOURNAL 12477932
 PUBMED 2 (bases 1 to 4254)
 REFERENCE Strausberg, R.
 AUTHORS Direct Submission
 JOURNAL Submitted (30-JUL-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT On Aug 19, 2003 this sequence version replaced gi:15079698.
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@hpgri.nih.gov
 Akheri, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Boufard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R.,
 Maduro, O.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Stantiripol, S., Thomas, P.J., Touchman, J.W.,
 Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.
 Clone distribution: MGC clone distribution information can be found
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 Series: IRML Plate: 26 Row: 3 Column: 2
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Similarity but not
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Query Match 100.0%; Score 400; DB 9; Length 4254;
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